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OM protein - protein search, using sw model.

Run on: May 2, 2006, 17:23:01 ; Search time 187 Seconds
 (without alignment)
 126.879 Million cell updates/sec

Title: US-10-644-927-1

Perfect score: 304

Sequence: 1 KTYGTGNGVHCTKNSLWGKV GRLQDILGWTAGFKTFH 54

Scoring table: BLASTM62
 Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Result No.	Score	Query Match	Length	DB ID	Description
1	304	100.0	54	AEB18127	Lactobaci
2	69.5	22.9	420	ADA33974	Acinetobaci
3	64	21.1	61	AAW17990	Sakacina P
4	62.5	20.6	558	ADR89438	crybun2-o
5	62	20.4	42	AAW1633	Lactobaci
6	60	19.7	37	AAW66446	Cationic
7	60	19.7	37	AYY91745	Porkhilenko V. D.
8	60	19.7	300	ARR6481	LEVCHUK V. P.
9	60	19.7	300	AAW37928	BORZENKOV V. N.
10	60	19.7	300	AAB69069	Svetoch O. E.
11	60	19.7	300	ABG1817	MITSEVICH E. V.
12	60	19.7	300	ABU09711	MITSEVICH I. P.
13	60	19.7	300	ABU09714	CD38 prot
14	60	19.7	300	ADD19904	Human dis
15	60	19.7	300	ADD45262	Human Pro
16	60	19.7	300	ADN40030	Cancer/
17	60	19.7	300	ADM32177	Human CD3
18	60	19.7	300	ADQ59526	Human can
19	60	19.7	300	ADQ88192	Human 903
20	60	19.7	300	ADY15608	PRO polyp
21	60	19.7	300	ADY19608	Ady19608 PRO polyp
22	60	19.7	300	AUZ13907	Human can
23	60	19.7	688	ABC06883	Novel hum
24	59.5	19.6	513	AAW79755	Euphorbia

ALIGNMENTS

RESULT 1
 AEB18127
 ID AEB18127 standard; protein; 54 AA.
 XX
 AC
 XX
 DT 22-SEP-2005 (first entry)

XX
 Lactobacillus salivarius strain PVD32 bacteriocin, OR7, SEQ ID NO:1.
 DE
 XX
 KW Bacteriocin; feedstuff; therapeutic; gene therapy; lactocin.
 XX
 Lactobacillus salivarius; strain PVD32.
 OS
 XX
 PN US2005153881-A1.
 XX
 PD 14-JUL-2005.
 XX
 PF 21-AUG-2003; 2003US-00644927.
 XX
 PR 21-AUG-2003; 2003US-00644927.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%	Query	Match	Length	DB	ID	Description
1	304	100.0	54	9	AEB18127	Lactobaci
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5	62	20.4	42	2	AAW1633	Lactobaci
6	60	19.7	37	2	AAW66446	Cationic
7	60	19.7	37	3	AYY91745	Porkhilenko V. D.
8	60	19.7	300	2	ARR6481	LEVCHUK V. P.
9	60	19.7	300	7	AAW37928	BORZENKOV V. N.
10	60	19.7	300	4	AAB69069	Svetoch O. E.
11	60	19.7	300	5	ABG1817	MITSEVICH E. V.
12	60	19.7	300	6	ABU09711	MITSEVICH I. P.
13	60	19.7	300	6	ABU09714	CD38 prot
14	60	19.7	300	7	ADD19904	Human dis
15	60	19.7	300	7	ADD45262	Human Pro
16	60	19.7	300	7	ADN40030	Cancer/
17	60	19.7	300	8	ADM32177	Human CD3
18	60	19.7	300	8	ADQ59526	Human can
19	60	19.7	300	8	ADQ88192	Human 903
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23	60	19.7	688	4	ABC06883	Novel hum
24	59.5	19.6	513	2	AAW79755	Euphorbia

AAU14564 Bacteriocin
 AAU91745 Brevicin,
 AAU91745 PA-1 bact
 AAU25078 PA-1 bact
 ABP09712 CD38 prot
 ABP23488 Bacteri
 ABP50093 GBL prote
 ADD64559 Trichodes
 ADD07160 Trichodes
 AEA00462 Inorganic
 ABB71088 Drosophil
 ABB71088 Protein e
 ABU44608 Protein e
 ABM69065 Photorhab
 ABM69065 Staphyloc
 ABP05473 Enterocin
 ABP04643 Bacteriop
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 ABB95053 E. faeciu
 ABP42656 Protein e
 ABP8314 Staphyloc
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AB

DE	Cationic peptide leukocin A-val 187.	PD	23-DEC-1999.
XX	Indolicidin analogue; resistance; cationic peptide; antibiotic;	XX	14-JUN-1999;
KW	bacterial infection; tolerance; antibacterial; microorganism; bacteria;	PF	98WO-CR000552.
KW	fungus; parasite; virus.	XX	12-JUN-1998;
XX	Leuconostoc gelidum.	PR	98US-00096541.
OS		XX	
XX	(MICR-) MICROLOGIX BIOTECH INC.	PA	(MICR-) MICROLOGIX BIOTECH INC.
PN	WO980401-A2.	XX	Friedland HD, Krieger TJ, Taylor R, Erflie D, Fraser JR, West MHP;
XX		XX	WPI; 2000-223549/19.
PD	17-SEP-1998.	DR	
XX	98WO-CA000190.	XX	Novel pharmaceutical composition containing optionally activated polyoxyalkylene-modified cationic peptides, useful for treating tumors.
PF	10-MAR-1998;	PT	This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon
XX	10-MAR-1997;	XX	
PR	97US-0040649P.	PS	Sequence 37 AA;
PR	20-AUG-1987;	XX	Query Match Score 60; DB 3; Length 37;
PR	97US-0091531P.	Best Local Similarity 48.4%; Pred. No. 4;	Best Local Similarity 48.4%; Pred. No. 4;
PR	26-SEP-1987;	Matches 15; Conservative 2; Mismatches 4;	Matches 15; Conservative 2; Mismatches 4;
PR	97US-0060099P.	Indels 10; Gaps 3;	Indels 10; Gaps 3;
XX	25-FEB-1998;	XX	
XX	98US-00030619.	Qy	3 YYGTNGVHCTKNSL--WGVV-----RLKN 24
PA	(MICR-) MICROLOGIX BIOTECH INC.	Db	2 YYG-NGVHCTKSGCSVNNGEAFSAGVHRLAN 31
XX	Fraser JR, West MHP, Monicoli PJ;	XX	
XX	WPI; 1998-5208080/44.	AC	RESULT 8
XX	New indolicidin peptide analogues - useful for, e.g. enhancing activity	XX	AAR56481
PT	of antibiotic or overcoming tolerance, acquired resistance or inherent	XX	ID AAR56481 standard; protein; 300 AA.
PT	resistance of microorganisms.	AC	AAR56481;
XX	PS	XX	XX
PS	Sequence 37 AA;	AC	XX
PS	Disclosure; Page 11; 105PP; English.	XX	25-MAR-2003 (revised)
XX	AAW66393 to AAW66469 represent native cationic peptides from the present invention. The present invention describes compositions and methods for treating infection, especially bacterial infections. The compositions and methods use cationic peptides in combination with an antibiotic agent which are then administered to a patient to enhance the activity of the antibiotic agent, to overcome: (a) tolerance; (b) acquired resistance; and (c) inherent resistance. The combinations of antibiotics and cationic peptides can provide synergistic activity against a microorganism that is tolerant, inherently resistant, or has acquired resistance to an antibiotic agent. They can be used for killing e.g. bacteria, fungi, parasites and viruses	XX	DT 22-FEB-1995 (first entry)
XX	SQ	XX	XX
XX	CC	CD38.	XX
CC	AAW66393 to AAW66469 represent native cationic peptides from the present invention. The present invention describes compositions and methods for treating infection, especially bacterial infections. The compositions and methods use cationic peptides in combination with an antibiotic agent which are then administered to a patient to enhance the activity of the antibiotic agent, to overcome: (a) tolerance; (b) acquired resistance; and (c) inherent resistance. The combinations of antibiotics and cationic peptides can provide synergistic activity against a microorganism that is tolerant, inherently resistant, or has acquired resistance to an antibiotic agent. They can be used for killing e.g. bacteria, fungi, parasites and viruses	DB	CD38; therapeutic; diagnostic.
CC	CC	XX	KW
CC	CC	OS	OS
CC	CC	XX	Homo sapiens.
CC	CC	PN	W0941784-A1.
CC	CC	XX	
XX	XX	XX	XX
XX	XX	XX	04-AUG-1994.
XX	XX	XX	04-AUG-1994.
XX	XX	XX	27-JAN-1994;
AC	AAV91745 standard; peptide; 37 AA.	XX	94WO-US000517.
AC	AAV91745;	XX	
DT	06-JUN-2000 (first entry)	PR	29-JAN-1993;
XX		XX	93US-00010905.
XX	Cationic peptide Leukocin A-val 187 amino acid sequence.	PA	(SCHE) SCHERRING CORP.
XX		PA	PA (STRD) UNIV LEELAND STANFORD JUNIOR.
KW	Cationic peptide; tumour; pharmaceutical composition; cancer; treatment;	XX	Parkhouse RME, Santos-Argumedo L, Grimaldi JC, Bazan JF, Heath A;
KW	leukaemia; polyoxyalkylene-modified; APO; lymphoma; multiple myeloma;	PI	Howard MC, Goodnow CC;
KW	breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;	PI	
KW	multidrug resistance.	XX	WPI; 1994-264098/32.
XX	Unidentified.	DR	N PSDLB; AAC0644.
OS		XX	Modulation of responses of lymphocytes - using antibody to CD38, a soluble CD38 fragment or a modulator of ADP-ribosyl cyclase or cyclic ADP
PN	W09965506-A2.	PT	-ribosyl hydrolase.
XX		PT	

ID	AAB69069	standard; protein; 300 AA.
PS	XX	XX
CC	The protein is a human CD38 molecule which is used to modulate the physiological response of a lymphocyte, which is useful for the stimulation/inhibition of lymphocyte growth or differentiation, particularly for the establishment of antigen tolerance. (Updated on 25-MAR-2003 to correct PN field.)	XX
CC	Sequence 300 AA;	XX
SQ	<p>Query Match 19.7%; Score 60; DB 2; Length 300;</p> <p>Best Local Similarity 35.0%; Pred. No. 49;</p> <p>Matches 14; Conservative 7; Mismatches 19; Indels 0; Gaps 0;</p> <p>Qy 5 GTNGVHCTKNSLWKGVRILKMKYDQNTTYMGRQLDILGW 44</p> <p>Db 113 GTQTPCNCNKLLWSRIKDLAHQFTQVQRDMETFLDTLGY 152</p>	OS Homo sapiens.
RESULT 9		XX
ID	AAW37928	standard; protein; 300 AA.
XX	XX	JP2000316578-A.
AC	AAW37928;	PN XX
XX	XX	DE 21-NOV-2000.
DT	09-SEP-1998	PD XX
XX	XX	PF 12-MAY-1999;
DE	Amino acid sequence of CD38.	XX
XX	XX	PR 12-MAY-1999; 99JJP-00131955.
KW	CD38; CD38 peptide fragment; anti-CD38 autoantibody; autoimmune disease; insulin dependent diabetes mellitus; type II diabetes.	XX
XX	XX	PA (BMLB-) BML KK.
OS	Mammalia.	PA (KANE/) KANETSUKA A.
XX	XX	PA (OKAM/) OKAMOTO H.
PN	WO9816245-A1.	XX
XX	XX	DR 2001-128255/14.
PD	23-APR-1998.	N-PSDB; AAF32487.
XX	XX	XX
PF	11-APR-1997; 97WO-JP001259.	XX
XX	XX	XX
PF	15-OCT-1996; 96JJP-0022537.	XX
XX	XX	XX
(SHIO) SHIONOGI & CO LTD.	PA	XX
XX	Taminato T;	XX
PI	WPI; 1998-251054/22.	XX
XX	DR N-PSDB; AAV29155.	XX
PT	Assaying anti-CD38 auto-antibody - useful for detecting auto-immune disease, e.g. type II diabetes.	XX
XX	DISCLOSURE: Page 8-10; 17pp; Japanese.	XX
PS	This is the amino acid sequence of the CD38 protein, of which a fragment is used in the method of the invention to create the anti-CD38 autoantibody. The method is used for detecting autoimmune disease, e.g. insulin dependent diabetes mellitus or type II diabetes	XX
SQ	Sequence 300 AA;	XX
RESULT 11		XX
ID	ABG61817	standard; protein; 300 AA.
XX	XX	PN WO200230268-A2.
AC	ABG61817;	XX
XX	XX	PR 15-AUG-2002 (First entry)
XX	XX	DE 15-AUG-2002.
XX	XX	Prostate cancer-associated protein #18.
XX	XX	XX
XX	Prostate cancer; prostate tumour tissue; human; mammal; cytosatic.	XX
OS	Mammalia.	XX
XX	XX	PD 18-APR-2002.
XX	XX	PR 12-OCT-2001; 2001WO-US032045.
XX	XX	PF 08-DEC-2000; 2000US-00687576.
PR	13-OCT-2000; 2000US-0073288.	XX
PR	08-DEC-2000; 2000US-00733742.	XX
PR	24-JAN-2001; 2001US-0263957P.	PR
RESULT 10		
ID	AAB69069	

PI Kanatsuka A, Takasawa S, Okamoto H;
 XX WPI; 2003-417248/39.

PT Detecting risk factor for onset of diabetes in an individual, involves
 PT detecting genetic abnormality of the gene CD38.
 XX Example; Page: 29pp; English.

XX The invention describes a method of detecting a risk factor for diabetic
 CC onset in an individual. The method involves detecting genetic abnormality
 CC of the gene CD38 which is a human lymphocyte surface marker and is a risk
 CC gene for onset of diabetes. The sites of abnormality in CD38 gene include
 CC a site encoding Arg at residue 140, a site encoding Ser at residue 264,
 CC or guanine at nucleotide position -28 in intron 7. This is the amino acid
 CC sequence of CD38 protein S264L mutant that results from a mutation in the
 CC gene encoding CD38, a risk factor in the onset of diabetes

SQ Sequence 300 AA;

Query Match 19.7%; Score 60; DB 6; Length 300;
 Best Local Similarity 35.0%; Pred. No. 49;
 Matches 14; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 5 GTNGVHCTKNSLWKGKVRLKMKYDONTTYNGRLQDILGW 44
 DB 113 GTQTVPCNKLWLSRKIDLAHQFTQVQRDMFTEDTLGY 152

RESULT 14
 ADD18904 standard; protein; 300 AA.

XX ADD18904;
 AC ADD18904;
 DT 15-JAN-2004 (First entry)
 XX Human disease related protein SeqID393.

DE human; disease state; cyostatic; antiinflammatory; ophthalmological;
 KW antiarteriosclerotic; vulnerary; gene therapy;
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 KW inflammation; erythropoiesis; glycolysis; Gluconeogenesis;
 KW glucose transport; catecholamine synthesis; iron transport;
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 KW inflammatory condition; wound healing.

XX Homo sapiens.

OS WO2003018621-A2.

XX PD 06-MAR-2003.

PF 23-AUG-2002; 2002WO-GB003892.

XX PR 23-AUG-2001; 2001GB-00020558.
 PR 05-OCT-2001; 2001GB-00024037.

XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.

XX PI Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
 XX DR 2003-290046/28.
 DR N-PSDB; ADD18905.

PT New substantially purified polypeptide, useful for diagnosing or treating
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
 PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 PT wound healing.

XX PS Claim 25; SEQ ID NO 393; 424pp; English.

XX PS Sequence 300 AA;

Query Match 19.7%; Score 60; DB 7; Length 300;
 Best Local Similarity 35.0%; Pred. No. 49;
 Matches 14; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 5 GTNGVHCTKNSLWKGKVRLKMKYDONTTYNGRLQDILGW 44
 DB 113 GTQTVPCNKLWLSRKIDLAHQFTQVQRDMFTEDTLGY 152

RESULT 15
 ADD45262 standard; protein; 300 AA.

XX ID ADD45262;
 AC ADD45262;
 DT 29-JAN-2004 (first entry)
 XX Human Protein P28907, SEQ ID NO 10695.

XX DE Human; pain; neuronal tissue; gene therapy;
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SN; Chung.

XX Homo sapiens.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US035765.

XX PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-034382P.
 PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;
 XX DR WPI; 2003-268312/26.
 DR GENBANK; P28907.

XX PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page: 101pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g., spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. Gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences.

XX Sequence 300 AA;

Query Match 19.7%; Score 60; DB 7; Length 300;
Best Local Similarity 35.0%; Pred. No. 49;
Matches 14; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 5 GTNGVACTNSLWGVRLKRMKYDNTTNGRLDILIGW 44
Db 113 GTQTVPCNKKLWSRKLDAHQFTQVRDMFTLEDILGY 152

Search completed: May 2, 2006, 17:26:33
Job time : 191 secs

Run on:	May 2, 2006, 17:26:51 ; Search time 38 Seconds (without alignments) 136.729 Million cell updates/sec	30	54	17.8	494	2	JC2392
Title:	US-10-644-927-1	31	53.5	17.6	324	2	S31393
Perfect score:	304	32	53.5	17.6	462	1	G69515
Sequence:	1 KTYYGTVHCTKNSLWGKV.....GRLQDILGWATGAFGKTFH 54	33	53.5	17.6	510	2	YSBTM
Scoring table:	BLOSUM62	34	53.5	17.6	527	2	D84610
Searched:	Gapop 10.0 , Gapext 0.5	35	53.5	17.6	1091	1	PL0009
Total number of hits satisfying chosen parameters:	283416	36	53.5	17.6	1166	2	Gene 12 protein -
Minimum DB seq length:	0	37	53.5	17.6	1585	2	complement C3d/Eps
Maximum DB seq length:	2000000000	38	53.5	17.6	1585	2	hypothetical prote
Post-processing:	Minimum Match 0 [*]	39	53	17.4	167	2	FUN81 protein -
	Maximum Match 100 [*]	40	53	17.4	202	2	phage-related prot
Database :	PIR 80:*	41	53	17.4	249	2	probable myo-inosi
	1: Pirl1:*	42	53	17.4	258	2	thronine-tRNA lig
	2: Pir2:*	43	53	17.4	264	2	Gene 12 protein -
	3: Pir3:*	44	53	17.4	327	2	probable nucleosid
	4: Pir4:*	45	53	17.4	327	2	tail fiber protein
							TOM37 protein - ye
							cellulase (EC 3.2.
							glutathione transf
							tail fiber adhesin
							EC 3.2.
							TOM37 protein - ye
							sodium/proline sym
							chlorophyll a/b-pro
							transcription regu
							lign
							probable myo-inosi
							Gene 12 protein -
							complement C3d/Eps
							hypothetical prote
							phage-related prot
							FUN81 protein -
							probable myo-inosi
							thronine-tRNA lig
							Gene 12 protein -
							probable nucleosid
							tail fiber protein
							hypothetical prote
							tail fiber adhesin
							EC 3.2.
							glutathione transf
							TOM37 protein - ye
							sodium/proline sym
							chlorophyll a/b-pro
							transcription regu
							lign
							probable myo-inosi
							Gene 12 protein -
							complement C3d/Eps
							hypothetical prote
							phage-related prot
							FUN81 protein -
							probable myo-inosi
							thronine-tRNA lig
							Gene 12 protein -
							probable nucleosid
							tail fiber protein
							hypothetical prote
							tail fiber adhesin
							EC 3.2.
							glutathione transf
							TOM37 protein - ye
							sodium/proline sym
							chlorophyll a/b-pro
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							Gene 12 protein -
							complement C3d/Eps
							hypothetical prote
							phage-related prot
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							probable myo-inosi
							thronine-tRNA lig
							Gene 12 protein -
							probable nucleosid
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							tail fiber adhesin
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							glutathione transf
							TOM37 protein - ye
							sodium/proline sym
							chlorophyll a/b-pro
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							Gene 12 protein -
							complement C3d/Eps
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							probable myo-inosi
							thronine-tRNA lig
							Gene 12 protein -
							probable nucleosid
							tail fiber protein
							hypothetical prote
							tail fiber adhesin
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							glutathione transf
							TOM37 protein - ye
							sodium/proline sym
							chlorophyll a/b-pro
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							probable myo-inosi
							Gene 12 protein -
							complement C3d/Eps
							hypothetical prote
							phage-related prot
							FUN81 protein -
							probable myo-inosi
							thronine-tRNA lig
							Gene 12 protein -
							probable nucleosid
							tail fiber protein
							hypothetical prote
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							glutathione transf
							TOM37 protein - ye
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							Gene 12 protein -
							complement C3d/Eps
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							thronine-tRNA lig
							Gene 12 protein -
							probable nucleosid
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							chlorophyll a/b-pro
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							complement C3d/Eps
							hypothetical prote
							phage-related prot
							FUN81 protein -
							probable myo-inosi
							thronine-tRNA lig
							Gene 12 protein -
							probable nucleosid
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							hypothetical prote
							tail fiber adhesin
							EC 3.2.
							glutathione transf
							TOM37 protein - ye
							sodium/proline sym
							chlorophyll a/b-pro
							transcription regu
							lign
							probable myo-inosi
							Gene 12 protein -
							complement C3d/Eps
							hypothetical prote
							phage-related prot
							FUN81 protein -
							probable myo-inosi
							thronine-tRNA lig
							Gene 12 protein -
							probable nucleosid
							tail fiber protein
							hypothetical prote
							tail fiber adhesin
							EC 3.2.
							glutathione transf
							TOM37 protein - ye
							sodium/proline sym
							chlorophyll a/b-pro
							transcription regu
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							probable myo-inosi
							Gene 12 protein -
							complement C3d/Eps
							hypothetical prote
							phage-related prot
							FUN81 protein -
							probable myo-inosi
							thronine-tRNA lig
							Gene 12 protein -
							probable nucleosid
							tail fiber protein
							hypothetical prote
							tail fiber adhesin
							EC 3.2.
							glutathione transf
							TOM37 protein - ye
							sodium/proline sym
							chlorophyll a/b-pro
							transcription regu
							lign
							probable myo-inosi
							Gene 12 protein -
							complement C3d/Eps
							hypothetical prote
							phage-related prot
							FUN81 protein -
							probable myo-inosi
							thronine-tRNA lig
							Gene 12 protein -
							probable nucleosid
							tail fiber protein
							hypothetical prote
							tail fiber adhesin
							EC 3.2.
							glutathione transf
							TOM37 protein - ye
							sodium/proline sym
							chlorophyll a/b-pro
							transcription regu
							lign
							probable myo-inosi
							Gene 12 protein -
							complement C3d/Eps
							hypothetical prote
							phage-related prot
							FUN81 protein -
							probable myo-inosi
							thronine-tRNA lig
							Gene 12 protein -
							probable nucleosid
							tail fiber protein
							hypothetical prote
							tail fiber adhesin
							EC 3.2.
							glutathione transf
							TOM37 protein - ye
							sodium/proline sym
							chlorophyll a/b-pro
							transcription regu
							lign
							probable myo-inosi
							Gene 12 protein -
				</td			

1 KTYGTN--GVHCTKNSLWGKVRLKOMKVDONTY 33
 255 KPIYDGTCGMH--THLSLWTKDGRKRNLMVDPNDEY 288

RESULT 3

S38508 sakacin P precursor - Lactobacillus sake (strains Lb674 and Lm673)
 C;Species: Lactobacillus sake
 A;Variety: strains Lb 674 and Lm 673
 C;Date: 25-Dec-1994 #sequence_change 13-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S57911; S57915; S43689; S38508
 R;Holck, A.; Holck, A.; Axelson, L.; Kroekel, L.
 Submitted to the EMBL Data Library, February 1995
 A;Description: Purification and cloning of sakacin 674, a bacteriocin from Lactobacillus
 A;Reference number: S57910
 A;Accession: S57911
 A;Molecule type: DNA
 A;Residues: 1-61 <HUE>
 A;Cross-references: UNIPROT:P35618; UNIPARC:UPI00000013AD; EMBL:Z48542; NID:9695615; PID:
 A;Experimental source: strain Lb674
 R;Holck, A.L.; Axelson, L.; Huelne, K.; Kroekel, L.
 FEMS Microbiol. Lett. 115, 143-150, 1994
 A;Title: Purification and cloning of sakacin 674, a bacteriocin from Lactobacillus sake
 A;Reference number: S57915; MUID:9418610; PMID:8138128
 A;Accession: S57915
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-61 <HOL>
 A;Cross-references: UNIPARC:UPI00000013AD; EMBL:Z225816; NID:g414124; PIDN:CAA81064_1; PI:
 A;Experimental source: strain Lb674
 R;Richaere, P.S.; Vogel, R.F.; Hammes, W.P.
 Microbiology 140, 361-367, 1994
 A;Title: Cloning and sequencing of sakP encoding sakacin P, the bacteriocin produced by
 A;Accession: S43689
 A;Molecule type: DNA
 A;Residues: 1-61 <TIC>
 A;Cross-references: UNIPARC:UPI00000013AD; EMBL:X75081; NID:g475950; PIDN:CAAS2974_1; PI:
 A;Experimental source: strain Lm 673
 C;Keywords: antibiotic; bacteriocin
 F;1-18/Domain: propeptide #status predicted <PRO>
 F;19-61/Product: sakacin P #status predicted <MAT>
 F;27-32/Disulfide bonds: #status predicted

Query Match 21-1% Score 64 DB 1; Length 61;
 Best Local Similarity 36.7%; Pred. No. 0.31; Indels 9; Gaps 4;
 Matches 18; conservative 4; Mismatches 9;

Qy 3 YYGTTGVTCTKNSL--WGKVRLKOMKVDONTYMGRL-QDILIGWATG 47
 Db 20 YYG-NGVHCTKNSLWGSCTWDKG-----TAIGNGRNAAANWATG 54

RESULT 4

AP2555 hypothetical protein a118037 [Imported] - *Nostoc* sp. (strain PCC 7120) plasmid pCC7120g
 C;Species: *Nostoc* sp. PCC 7120
 A;Note: *Nostoc* sp. Strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_change 14-Dec-2001 #text_change 09-Jul-2004
 C;Accession: AP2555
 R;Kaneko, T.; Nakamura, Y.; Wolf, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, S.; Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.; DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. AP2555
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AP2555
 A;Status: Preliminary
 A;Molecule type: DNA

A;Residues: 1-590 <KUR>
 A;Cross-references: UNIPROT:Q8YK80; UNIPARC:UPI00000CEFF0;
 A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: a118037
 A;Genome: plasmid

Query Match 20.7% Score 63; DB 2; Length 590;
 Best Local Similarity 35.3%; Pred. No. 5.4%;
 Matches 23; Indels 2; Gaps 1;

Qy 3 YYGTTGVTCTKNSLWGSCTWDKG-----TAIGNGRNAAANWATG 47
 Db 88 YYG-T-PRGTFQVGNKRITNPEDKNRLLPDYQRGLVSGSGGSGKTF 136

RESULT 5

A43995 Glutamate-ammonia ligase (EC 6.3.1.2) - *Methanococcus voltae*
 C;Species: Methanococcus voltae
 C;Date: 11-Feb-1993 #sequence_change 11-Feb-1993 #text_change 09-Jul-2004
 C;Accession: A43995; S13504
 R;Pisot, O.; Sibold, L.; Aubert, J.P.
 Res. Microbiol. 140, 355-371, 1989
 A;Title: Nucleotide sequence and expression of the glutamine synthetase structural gene,
 A;Reference number: A43995; MUID:9019872; PMID:257777
 A;Accession: A43995
 A;Molecule type: DNA
 A;Residues: 1-446 <POS>
 A;Cross-references: UNIPROT:221154; UNIPARC:UPI000012B6EC; GB:X53509; NID:944711; PIDN:C
 A;Gene: glnA
 C;Keywords: glutamate-ammonia ligase

Query Match 20.6% Score 62.5; DB 2; Length 446;
 Best Local Similarity 33.9%; Pred. No. 4.5%;
 Matches 19; Conservative 9; Mismatches 17; Indels 11; Gaps 5;

Qy 1 KTYGTN--GVHCTKNSLW--GVYRKNNKMYKDONTYMGRL-QDILIGWATGAFKT 52
 Db 237 KPFFGMNSGMHCNQ-SIWLDGKPSF---YDENNAH--QSLSDICLTSYGGILEHT 285

RESULT 6

A41657 leucocin A-UAL 187 precursor - Leuconostoc gelidum plasmid pLG7.6
 C;Species: Leuconostoc gelidum
 C;Accession: A41657
 R;Hastings, J.W.; Sailer, M.; Johnson, K.; Roy, K.L.; Vedras, J.C.; Stiles, M.E.
 J. Bacteriol. 173, 7491-7500, 1991
 A;Title: Characterization of leucocin A-UAL 187 and cloning of the bacteriocin gene from
 A;Reference number: A41657; MUID:92041660; PMID:1840587
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-61 <HAS>
 C;Keywords: carnobacteriocin precursor
 C;Keywords: antibiotic; bacteriocin
 F;1-18/Domain: propeptide #status predicted <PRO>
 F;19-61/Product: sakacin P #status predicted <MAT>
 F;27-32/Disulfide bonds: #status predicted

Query Match 21.1% Score 64 DB 1; Length 61;
 Best Local Similarity 36.7%; Pred. No. 0.31; Indels 9; Gaps 4;

Qy 3 YYGTTGVTCTKNSL--WGKVRLKOMKVDONTYMGRL-QDILIGWATG 47
 Db 20 YYG-NGVHCTKNSLWGSCTWDKG-----TAIGNGRNAAANWATG 54

RESULT 7

RES5555 hypothetical protein a118037 [Imported] - *Nostoc* sp. (strain PCC 7120) plasmid pCC7120g
 C;Species: *Nostoc* sp. Strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_change 14-Dec-2001 #text_change 09-Jul-2004
 C;Accession: AP2555
 R;Kaneko, T.; Nakamura, Y.; Wolf, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, S.; Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.; DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. AP2555
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AP2555
 A;Status: Preliminary
 A;Molecule type: DNA

Query Match 19.7% Score 60; DB 2; Length 61;
 Best Local Similarity 48.4%; Pred. No. 1; Mismatches 2; Indels 4; Gaps 3;

Qy 3 YYGTTGVTCTKNSL--WGKVRLKOMKVDONTYMGRL-QDILIGWATG 47
 Db 26 YYG-NGVHCTKNSLWGSCTWDKG-----TAIGNGRNAAANWATG 54

P;19-62/Product: pediocin PA-1 #status experimental <MAT>
 P;27-32,42-62/Disulfide bonds: #status experimental

Query Match Score 19.4%; DB 1; Length 62;
 Best Local Similarity 37.5%; Pred. No. 1.4;
 Matches 18; Conservative 5; Mismatches 9; Indels 8 4;
 Gaps 16;

Qy 3 YYGTNGVHCTKNSL---WGVRLKNNMKYDQNTTYMGRQLDILGWTG 47
 Db 20 YYG-NGVTGKHSCTSVWGRA-----TTCT--INGAMAWATG 54

RESULT 11

T20455
 hypothetical protein F01DA_3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Jul-2004
 C;Accession: T20455
 R;Wild, A.
 Submitted to the EMBL Data Library, October 1996
 A;Reference number: Z12278
 A;Accession: T20455
 A;Status: Preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-399 <WIL>
 A;Cross-references: UNIPROT:O17755; UNIPARC:UPI000007E797; EMBL:Z81054; PIDN:CAB02882.1;
 A;Experimental source: Clone F01DA
 A;Map position: 4
 A;Introns: 45/3; 235/2; 294/2

Query Match Score 19.4%; DB 2; Length 399;
 Best Local Similarity 33.8%; Pred. No. 11;
 Matches 19; Conservative 4; Mismatches 22; Indels 8; Gaps 3;

Qy 3 YYGTNGVHCTKNSLWGVRLKNNMKYDQNTTYMGRQLDILGWTG 53
 Db 75 YYTDNSGSNN---GFRFLKNPILQQPEWYMH---SDVTPAGKVIGEGAFRKVP 121

RESULT 12

T18995
 hypothetical protein C06B8_7 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 R;Steward, C
 Submitted to the EMBL Data Library, November 1996
 A;Reference number: Z19057
 A;Accession: T18995
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-3036 <WIL>
 A;Cross-references: UNIPROT:O17575; UNIPARC:UPI000017B740; EMBL:Z81463; PIDN:CAB03852.1;
 A;Experimental source: clone C06B8
 C;Genetics:

Query Match Score 19.1%; DB 2; Length 3036;
 Best Local Similarity 26.1%; Pred. No. 1.5e+02;
 Matches 18; Conservative 5; Mismatches 25; Indels 22; Gaps 2;

Qy 1 KTYGTNGVHCT-----KNSLWGKVRLKNNMKYDQNTTYMGRL-----Q 38
 Db 543 KAYGLNVNCIIRRNTGNGVFANDIRETALTNVTLDENOQTAGFLYRDGAIDIWNET 602

RESULT 13

T50021
 inositol-3-phosphate synthase (EC 5.5.1.4) T31P16.160 [similarity] - Arabidopsis thaliana
 N;Alternate names: protein T31P16.160
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C;Accession: T50021
 R;Bevan, M.; Zimmermann, W.; Grueisen, A.; Wambutt, R.; Kalicki, J.; Wohldmann, P.; Smits, submitted to the Protein Sequence Database, May 2000
 A;Reference number: 225027
 A;Accession: T50021
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-510 <BEV>
 A;Cross-references: UNIPROT:Q9LX12; UNIPARC:UPI000001794; EMBL:T31P16
 A;Experimental source: cultivar Columbia; BAC clone T31P16
 C;Genetics:
 A;Gene: ATSP-T31P16.160
 A;Map Position: 5
 A;Introns: 63/2; 86/2; 131/3; 214/2; 290/1; 328/3; 387/3; 450/3; 471/3
 C;Superfamily: myo-inositol-1-phosphate synthase
 C;Keywords: intramolecular lyase; isomerase; NAD

Query Match Score 18.9%; DB 2; Length 510;
 Best Local Similarity 37.7%; Pred. No. 23;
 Matches 20; Conservative 8; Mismatches 20; Indels 5; Gaps 4;

Qy 3 YYGTNGVHCTKNSL-WGVRLKNNMKYDQNTTYMGRQLDILGWTGAFGKT 52
 Db 26 YQTTELVHENKNGAQN-TVKEPATVKEFKTDTHPKLGVMLVGWG-GNNGST 76

RESULT 14

GIBPT4
 gene 12 protein - phage T4
 N;Alternate names: tail fiber protein
 C;Species: Phage T4
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 30-Jun-1993
 C;Accession: S01889
 R;Belivanov, N.A.; Prilipov, A.G.; Mesyanzhinov, V.V.

Query Match Score 18.6%; DB 1; Length 517;
 Best Local Similarity 33.3%; Pred. No. 31;
 Matches 15; Conservative 8; Mismatches 15; Indels 7; Gaps 2;

Qy 8 GVRCTKNSLWGKVRLKNNMKYDQNTTYMGRQLDILGWTGAFGKT 52
 Db 416 GVGCTGGXY-GEVQIQOMSYKHAGGFGEHDDL----GAFONT 453

RESULT 15

PC2131
 hepatocyte growth factor receptor - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004
 C;Accession: PC2131
 R;Teruiji, M.; Kawano, S.; Tsuji, S.; Ito, T.; Hayashi, N.; Horimoto, M.; Mita, E.; Nagano, Biophys. Res. Commun. 200, 536-541, 1994
 Biochem. A;Title: Increased expression of C-met messenger RNA following acute gastric injury in rat
 A;Reference number: PC2131; MUID:94220137; PMID:8166728

A;Accession: PC2131
A;Molecule type: mRNA
A;Residues: 1-132 <TSU>
A;Cross-references: UNIPARC:P97523; UNIPROT:UPI0000170C8C; GB:S69881; NID:9516427; PIDN:
C;Comment: This protein participates in the healing process of gastric mucosa after inju
C;Genetics:
A;Gene: c-met
C;Superfamily: Tyrosine-protein kinase, HGF/MSP receptor type; protein kinase homology
C;Keywords: ATP; receptor

Query Match 18.3%; Score 55 5; DB 2; Length 132;

Best Local Similarity 31.4%; Pred. No. 9.1;
Matches 16; Conservative 7; Mismatches 17; Indels 11; Gaps 2;

Qy 3 YYGNGVHC----TRANSIUMGRVFLRNKMYDQNTT-----YNCRLQDIL 42

Db 27 FYGPNHEHCFNRTLIRNSSGCEVRSDETYRTEFTALQRVDLFGRLNATWL 77

Search completed: May 2, 2006, 17:31:16
Job time : 41 secs

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ATTACHMENT

searched: 2166443 seqs, 705528306 residues
total number of hits satisfying chosen parameters: 2166443

minium DB seq length: 0
minium DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing First 45 summaries

database : UniProt_05_80:
 1: uniprot_sprot:*

2: uniprot_trembl:
 { Pred. No. is the number of results predicted by chance to

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query built No.	Score	Query		Length	DB	ID	Description
		Match	Start				
1	195	64.1	81	2	Q48496	LACAC	lactobacillus
2	65.5	21.5	471	1	GJNA	SU11SO	P23794 sullobacillus
3	65	21.4	301	1	CD38	_MACFA	Q5vano maceca fusc
4	65	21.4	325	2	Q5XQ46	_9PEZI	Q5XQ46 cryptococcus
5	64.5	21.2	460	2	QANH89	_9MICC	Q4nhs9 arthrobacter
6	64.5	21.2	1071	2	Q75CA6	_ASRGC	Q75CA6 ashyba goss
7	64	21.1	61	1	SAKP	_LACSK	P35618 lactobacilli
8	64	21.1	61	2	Q175	_LACSK	Q7b5f5 lactobacilli
9	64	21.1	714	2	Q51P75	_MAGGR	Q51p75 magnaporthe
10	63	20.7	590	2	Q8YK80	_ANASP	Q8yk80 anaerena sp
11	63	20.7	1582	2	Q8RIM1	_FUSNN	Q8rim1 fusobacteri
12	63	20.7	1630	2	QBHH7	_FUSNN	QBHH7 fusobacteri
13	62.5	20.6	446	1	GLNA	_METYVO	P21154 methanococc
14	62.5	20.6	558	2	BACTA	_W63	Q8vw63 bacillus th
15	61.5	20.2	469	2	Q9P203	_GVXN	Q9pz03 xestia c-nii
16	61.5	20.2	524	2	Q7QBD6	_ANOGA	Q7qed6 anopheles g
17	61.5	20.2	547	2	QBAJU6	_BACTN	Q8aij6 bacteroides
18	61.5	20.2	853	2	Q9D193	_9HIV1	Q9d193 human immun
19	61.5	20.2	858	2	Q9D179	_9HIV1	Q9d179 human immun
20	61.5	20.2	1474	2	Q4Q25Y	_LEIMA	Q4q25y leishmania
21	61	20.1	61	2	Q4U1B4	_LACCU	Q4u1b4 lactobacilli
22	61	20.1	684	2	Q5W164	_BACSK	Q5wi64 bacillus cl
23	61	20.1	1524	2	Q4U1Z1	_THEAN	P34u1z1 theilera a
24	60	19.7	61	1	LCCB	_LEUGE	P34034 leuconostoc
25	60	19.7	61	1	LCCB	_LEUCA	Q53446 leuconostoc
26	60	19.7	61	1	MTCV	_LEUME	P38577 leuconostoc
27	60	19.7	61	2	Q791V9	_LEUME	Q79iv9 leuconostoc
28	60	19.7	300	1	CD38	_HUMAN	P28907 homo sapien
29	60	19.7	498	2	Q622U2	_CAEBR	Q622u2 caenorhabdi
30	60	19.7	1143	2	Q948Y6	_VOLCA	Q948y6 volvox car
31	60	19.7	1754	2	QBRRH1	_FUSBACTERI	QBRRH1 fusobacteri

OX _TaxID=2287;
 RN [1] NUCLEOTIDE SEQUENCE; PubMed=1973523; DOI=10.1007/BF00261719;
 RX MEDLINE=20318316; PubMed=Barbarini A.M.; Barbarini D.; di Pasquale G.; Cammarano P.;
 RA Sanange-Lantoni A.M.; Barbarini D.; di Pasquale G.; Cammarano P.;
 RA Tiboni O.;
 RT "Cloning and nucleotide sequence of an archaeabacterial glutamine
 synthetase gene: phylogenetic implications.";
 RL Mol. Gen. Genet. 221:187-194(1990). ;
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX STRAIN=ATCC 35096 / DSM 161 / P2;
 RX MEDLINE=11332296; PubMed=111427726; DOI=10.1073/pnas.141220908;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Awavez C.-Y., Chau-Waiher C., Clausen T.G., Curtis B.A.,
 RA De Moors A., Brause G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozaera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schank M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle R.W., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sansen C.W., Van der Oost J.;
 RT Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001). ;
 CC -!- CATALYTIC ACTIVITY: ATP + L-glutamate + NH₃ = ADP + phosphate +
 CC L-glutamine.
 CC -!- ENZYME REGULATION: The activity of this enzyme is controlled by
 CC adenylylation under conditions of abundant glutamine. The fully
 CC adenylylated enzyme complex is inactive (By similarity).
 CC -!- SIMILARITY: Belongs to the glutamine synthetase family.
 CC -!
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 DR EMBL: X51263; CAA37353.1; -; Genomic_DNA.
 DR EMBL: X53263; CAA37352.1; -; Genomic_DNA.
 DR PIR: A99180; A99180.
 DR PIR: S11899; S11899.
 DR HSSP; P06201; LGRL.
 DR InterPro; IPR008147; Gln synt beta.
 DR InterPro; IPR008146; Gln synt_C.
 DR InterPro; IPR004809; GlnA.
 DR Pfam; PF00120; Gln synt_C; 1.
 DR Pfam; PF03951; Gln synt_N; 1.
 DR Prodom; PD001057; Gln synt_C; 1.
 DR TIGRFAM2; TIGR000653; GlnA; 1.
 DR PROSITE; PS00180; GlnA; 1.
 DR PROSITE; PS00181; GlnA_ATP; 1.
 KW Complete proteome; Ligase.
 FT BINDING 400 400 AMP (covalent) (By similarity).
 FT BINDING 162 162 S -> T (in Ref. 1).
 SQ SEQUENCE 471 AA; 53348 MW; 1C0423287B6C2CD CRC64;
 Query Match 21.5%; Score 65.5; DB 1; Length 471;
 Best Local Similarity 48.6%; Pred. No. 11; Indels 3; Gaps 2;
 Matches 17; Conservative 2; Mismatches 13; Indels 18; Gaps 0;
 Db 255 KTYYGTRN-SGVHCTKNSLGRVLRKMKYDQNTYGRLODILGW 33
 Db 255 KPIGDNGTGH-THLSLWTDKGRLNMIDPNDEY 288

OX _TaxID=CD38;
 RN Name=CD38;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 NCBI_TaxID=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RX PubMed=15383153; DOI=10.1186/1471-2172-5-21;
 RA Ferrero E., Orciani M., Vacca P., Ortolan E., Crovella S., Titti F.,
 RA Sacucci F., Malavasi F.;
 RT "Characterization and phylogenetic epitope mapping of CD38 ADPR cyclase in the cynomolgus macaque.";
 RL Immunol. 5:21-21 (2004).
 CC -!- FUNCTION: Synthesizes cyclic ADP-ribose, a second messenger for glucose-induced insulin secretion. Also has cADPR hydrolase activity. Also moonlights as a receptor system (By similarity).
 CC -!- CATALYTIC ACTIVITY: NAD(+)+ H(2)O = ADP-ribose + nicotinamide.
 CC -!- ENZYME REGULATION: ATP inhibits the hydrolyzing activity (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the ADP-ribosyl cyclase family.
 CC -!
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 CC -!
 DR EMBL; AY555148; AAT36330.1; -; mRNA.
 DR InterPro; IPR03193; Rib hydrolyse.
 DR PANTHER; PTHR10912; Rib Hydrolase; 1.
 DR Pfam; PF02267; Rib_hydrolase; 1.
 KW Glycoprotein; Hydrolase; NAD; Receptor; Signal-anchor; Transmembrane.
 FT TOPO_DOM 1 21 Cycloplasmic (Potential).
 FT TRANSMEM 22 43 Signal-anchor for type II membrane protein (Potential).
 FT FT Extracellular (Potential).
 FT ACT_SITE 4 4 301 By similarity.
 FT ACT_SITE 120 120 By similarity.
 FT CARBOHYD 202 202 By similarity.
 FT CARBOHYD 101 101 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 121 121 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 210 210 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 220 220 N-linked (GlcNAc. . .) (Potential).
 FT DISULFID 68 83 By similarity.
 FT DISULFID 100 181 By similarity.
 FT DISULFID 161 174 By similarity.
 FT DISULFID 255 276 By similarity.
 FT DISULFID 288 297 By similarity.
 SQ SEQUENCE 301 AA; 3442 MW; B659212B92616SB1 CRC64;
 Query Match 21.4%; Score 65; DB 1; Length 301;
 Best Local Similarity 35.0%; Pred. No. 8.1;
 Matches 14; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
 Oy 5 GTNSVHCTKNSLGRVLRKMKYDQNTYGRLODILGW 44
 Oy 114 GTQTVPCKNTLMSRKDLAHQFTVQRDMDFTLEDMLGY 153
 Oy RESULT 4
 Oy Q5XQ46_9PEZI PRELIMINARY; PRT; 325 AA.
 ID Q5XQ46_9PEZI
 AC Q5XQ46_9PEZI
 DT 25-OCT-2004 (TrEMBLrel.)
 DT 25-OCT-2004 (TrEMBLrel.)
 DT 25-OCT-2004 (TrEMBLrel.)
 DB Family 10 xylose isomerase (EC 3.2.1.8).
 OS Cryptovalsa sp. BCC 7197
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Xyariomycetidae; Xyariales; Diatrypaceae; Cryptovalsa.

OX NCBI_TaxID=295079;	Db 158 RSTRTGSGPHATRK-NKGAVILLIAVLGPWRETLAFQINILMGMIAADLLARNQRW 216
RN NUCLEOTIDE SEQUENCE.	Qy 45 ATGAGGKTF 53
RC STRAIN=BCC 7127;	Db 217 NQGFPGRGF 225
RA Boonyapakorn K., Pootanakit K., Chantasingh D., Kirtikara K.,	
RA Eurwilaichitr L.;	
RT "Cloning and expression of xylose 10 from Cryptosphaera sp. (BCC7197)	
RT in Pichia pastoris";	
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.	RESULT 6
DR EMBL; AY41212; AU98274.1; -; mRNA.	Q75CA6 ASHGO PRELIMINARY;
DR GO; GO:0031176; Fendo-1,4-beta-D-glucanase activity; IEA.	ID Q75CA6 ASHGO
DR GO; GO:0005975; P: carbohydrate metabolism; IEA.	AC Q75CA6;
DR InterPro; IPR001000; Glyco_hydro_10.	DT 05-TUL-2004 (TREMBrel. 27, Created)
DR Pfam; PF00331; Glyco_hydro_10; 1.	DT 05-TUL-2004 (TREMBrel. 27, Last sequence update)
DR PRINTS; PR0014; Glyclease.	DT 05-TUL-2004 (TREMBrel. 27, Last annotation update)
DR SMILES; SM00633; Glyco_10; 1.	DE ACRO6CP.
KW Glycosidase; Hydrolase; Xylan degradation.	GN Name=ACR006C;
SEQUENCE 325 AA; 35107 MW; 6E0930A/F8C6433C CRC64;	OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
Query Match Score 65; DB 2; Length 325;	OC Eukaryota; Fungi; Ascomycota; Saccaromycotina; Saccharomyces;
Best Local Similarity 32.8%; Pred. No. 8.9;	OC Saccharomycetidae; Saccharomyces; Eremothecium.
Matches 21; Conservative 6; Mismatches 15; Indels 22; Gaps 4;	NCBI_TaxID=33169;
Qy 1 KTYIGTNGVTCNKL-----WGVKVRULKN-MKXQDNTYMMGRILQ----DILL 42	RN [1]
Db 36 KLYYGT----CTDQGILTSQGSAALIQTQNFQVTSENNSKWDQTENSRGQFNLAQADLY 91	RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
Qy 43 GWAT 46	RC STRAIN=ATCC 10895;
Db 92 DWAT 95	RX PubMed=1500175; DOI=10.1126/science.1095781;
Query Match Score 65; DB 2; Length 460;	RA Dietrich F.S.; Voegeli S.; Brachatz S.; Lerch A.; Gates K.; Steiner S.;
Best Local Similarity 32.8%; Pred. No. 8.9;	RA Mohr C.; Poehmann R.; Luedi P.; Choi S.; Wing R.A.; Flavier A.;
Matches 21; Conservative 6; Mismatches 15; Indels 22; Gaps 4;	RA Gaffney T.D.; Philippson P.;
Qy 1 KTYIGTNGVTCNKL-----WGVKVRULKN-MKXQDNTYMMGRILQ----DILL 42	RT "The Ashbya gossypii genome as a tool for mapping the ancient
Db 36 KLYYGT----CTDQGILTSQGSAALIQTQNFQVTSENNSKWDQTENSRGQFNLAQADLY 91	RT Saccharomyces cerevisiae genome." /
Qy 43 GWAT 46	RL Science 304:304-307(2004);
Db 92 DWAT 95	DR BMBL; AE016816; AAS51233.1; -; Genomic_DNA.
Query Match Score 65; DB 2; Length 460;	DR AGD; ACR006C; -.
Best Local Similarity 32.8%; Pred. No. 8.9;	KW Complete proteome.
Matches 21; Conservative 6; Mismatches 15; Indels 22; Gaps 4;	SQ SEQUENCE 1071 AA; 123573 MW; 0816BS2D60032663 CRC64;
Qy 1 KTYIGTNGVTCNKL-----WGVKVRULKN-MKXQDNTYMMGRILQ----DILL 42	Query Match 21.2%; Score 64.5%; DB 2; Length 1071;
Db 36 KLYYGT----CTDQGILTSQGSAALIQTQNFQVTSENNSKWDQTENSRGQFNLAQADLY 91	AC Best Local Similarity 31.1%; Pred. No. 39; Mismatches 8; Matches 13; Conservative 8; Indels 9; Gaps 1;
Qy 43 GWAT 46	Qy 8 GVHCATNSLWGKVRLKMKYDQNTYMMGRLODILGWATGA 48
Db 92 DWAT 95	Db 702 GTAMAKXNSLIGCLSVHNKYEENAWYL-----WITSS 733
Query Match Score 65; DB 2; Length 460;	RESULT 7
Best Local Similarity 32.8%; Pred. No. 8.9;	SQ KAKP_LACSK STANDARD; PRT; 61 AA.
Matches 21; Conservative 6; Mismatches 15; Indels 22; Gaps 4;	AC ID KAKP_LACSK
Qy 1 KTYIGTNGVTCNKL-----WGVKVRULKN-MKXQDNTYMMGRILQ----DILL 42	AC P35678; Q57121;
Db 36 KLYYGT----CTDQGILTSQGSAALIQTQNFQVTSENNSKWDQTENSRGQFNLAQADLY 91	AC 01-JUN-1994 (Rel. 29, Created)
Qy 43 GWAT 46	DT 16-OCT-2001 (Rel. 40, Last sequence update)
Db 92 DWAT 95	DT 13-SEP-2005 (Rel. 48, Last annotation update)
Query Match Score 65; DB 2; Length 460;	DB Bacteriocin sakacin P precursor (Sakacin 674).
Best Local Similarity 32.8%; Pred. No. 8.9;	GN Name=sakP; Synonyms=sakR, sppa;
Matches 21; Conservative 6; Mismatches 15; Indels 22; Gaps 4;	OS Lactobacillus sakei.
Qy 1 KTYIGTNGVTCNKL-----WGVKVRULKN-MKXQDNTYMMGRILQ----DILL 42	OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Db 36 KLYYGT----CTDQGILTSQGSAALIQTQNFQVTSENNSKWDQTENSRGQFNLAQADLY 91	OC Lactobacillus.
Qy 43 GWAT 46	NCBI_TaxID=1599;
Db 92 DWAT 95	RN NUCLEOTIDE SEQUENCE.
Query Match Score 65; DB 2; Length 460;	RC STRAIN=FB24;
Best Local Similarity 32.8%; Pred. No. 8.9;	RC US DOE Joint Genome Institute (JGI-PG);
Matches 21; Conservative 6; Mismatches 15; Indels 22; Gaps 4;	RC Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Qy 1 KTYIGTNGVTCNKL-----WGVKVRULKN-MKXQDNTYMMGRILQ----DILL 42	RA Hamm N., Ierani S., Pittluck S., Richardson P.,
Db 36 KLYYGT----CTDQGILTSQGSAALIQTQNFQVTSENNSKWDQTENSRGQFNLAQADLY 91	RA "Annotation of the draft genome assembly of Arthrobacter sp. FB24." /
Qy 43 GWAT 46	RA "Sequencing of the draft genome assembly of Arthrobacter sp. FB24." /
Db 92 DWAT 95	RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
Query Match Score 65; DB 2; Length 460;	[2]
Best Local Similarity 32.8%; Pred. No. 8.9;	RP NUCLEOTIDE SEQUENCE.
Matches 21; Conservative 6; Mismatches 15; Indels 22; Gaps 4;	RC STRAIN=FB24;
Qy 1 KTYIGTNGVTCNKL-----WGVKVRULKN-MKXQDNTYMMGRILQ----DILL 42	RC Larimer F., Land M.;
Db 36 KLYYGT----CTDQGILTSQGSAALIQTQNFQVTSENNSKWDQTENSRGQFNLAQADLY 91	RC "Annotation of the draft genome assembly of Arthrobacter sp. FB24." /
Qy 43 GWAT 46	RC Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
Db 92 DWAT 95	CC -!- CAUTION: The sequence shown here is derived from an
Query Match Score 65; DB 2; Length 460;	CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
Best Local Similarity 32.8%; Pred. No. 8.9;	CC preliminary data.
Matches 21; Conservative 6; Mismatches 15; Indels 22; Gaps 4;	DR EMBL; AAGH01000004; EAL97009.1; -; Genomic_DNA.
Qy 1 KTYIGTNGVTCNKL-----WGVKVRULKN-MKXQDNTYMMGRILQ----DILL 42	KW Signal 460 Potential 1.
Db 36 KLYYGT----CTDQGILTSQGSAALIQTQNFQVTSENNSKWDQTENSRGQFNLAQADLY 91	FT SIGNAL 460 AA; 49805 MW; FSFB146AFB237113 CRC64;
Qy 43 GWAT 46	SQ SEQUENCE 460 AA; 49805 MW; FSFB146AFB237113 CRC64;
Db 92 DWAT 95	Query Match 21.2%; Score 64.5%; DB 2; Length 460;
Query Match Score 65; DB 2; Length 460;	Best Local Similarity 27.5%; Pred. No. 15; Mismatches 21; Indels 17; Gaps 3;
Best Local Similarity 27.5%; Pred. No. 15; Mismatches 21; Indels 17; Gaps 3;	Matches 19; Conservative 12; Mismatches 21; Indels 17; Gaps 3;
Qy 1 KTYIGTNGVTCNKL-----WGVKVRULKN-MKXQDNTYMMGRILQ----DILL 42	Qy 1 KTYIGTNGVTCNKL-----WGVKVRULKN-MKXQDNTYMMGRILQ----DILL 42

RL	PEMS Microbiol. Lett. 115:143-150 (1994).	RT	"Antimicrobial activity of lactic acid bacteria isolated from sour doughs; purification and characterization of bavaricin A, a bacteriocin produced by Lactobacillus bavaricus MI401.";
RN	[3]	RT	
RP	NUCLEOTIDE SEQUENCE.	RT	
RC	STRAIN=Lb674;	RT	
RX	MEDLINE=96262115; PubMed=8704983;	RL	J. Appl. Bacteriol. 75:113-122 (1993).
Huehne K., Axelsson L., Holck A., Kroekel L.;	RN		[2].
RT	"Analysis of the sakacin P gene cluster from Lactobacillus sake Lb674 and its expression in sakacin-negative Lb. sake strains."	RP	NUCLEOTIDE SEQUENCE.
RT	Microbiology 142:1437-1448 (1996).	RC	STRAIN=M1401;
RN	[4]	RA	Johansen A.H., Vogensen F.K.;
RP	PROTEIN SEQUENCE OF 19-59, AND CHARACTERIZATION.	RA	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
STRAIN=LTH673;	RC	RN	[3].
RA	Tichacek P.S., Nissen-Meyer J., Nes I.F., Vogel R.F., Hammes W.P.;	RP	NUCLEOTIDE SEQUENCE.
RT	"Characterization of the bacteriocins curvacin A from Lactobacillus curvatus LTH1174 and sakacin P from L. sake strain LTH673."	RC	STRAIN=N151;
RL	Syst. Appl. Microbiol. 15:460-465 (1992).	RA	Urgo R., Rantissio K., Cantoni C., Comi G., Luca C.;
CC	-1- FUNCTION: Bacteriocidal activity; inhibits closely related Lactobacilli, Listeria monocytogenes and ivanovii, Enterococcus faecalis, Carnobacterium sp and Brocotrix thermosphaeta.	RT	"Sequencing and expression analysis of the sakacin P bacteriocin produced by a Lactobacillus sake strain isolated from naturally fermented sausages."
CC	-1- SUBCELLULAR LOCATION: Secreted.	RT	Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
CC	-1- SIMILARITY: Belongs to the bacteriocin class IIAYGNGV family.	RL	Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
CC	This Swiss-Prot entry is copyright. It is produced through collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.	DR	EMBL; AP526262; AAM88838.1; -; Genomic DNA.
CC	-----	DR	EMBL; AF0022716; AA893970.1; -; Genomic DNA.
CC	-----	DR	EMBL; Z48542; CAA88028.1; -; Genomic DNA.
CC	-----	DR	EMBL; Z48516; CAA81064.1; -; Genomic DNA.
CC	-----	DR	PTR; SS7911; S38508.
CC	-----	DR	PDB; 10G7; NMR; A=19-61.
CC	-----	DR	PDB; 10HM; NMR; A=19-61.
CC	-----	DR	PDB; 10HN; NMR; A=19-61.
CC	-----	DR	InterPro: IPR002633: Bacteriocin_II.
CC	-----	DR	Pfam: PF01721; Bacteriocin_II.1.
CC	-----	DR	ProDom: PD00452; Bacteriocin_II.1.
CC	-----	DR	KW 3D-structure; Antibiotic; Antimicrobial; Bacteriocin;
CC	-----	DR	KW Direct protein sequencing.
CC	-----	FT	PROTPAP 1 18
CC	-----	FT	CHAIN 19 61
CC	-----	FT	Bacteriocin sakacin P.
CC	-----	FT	DISULFID 27 32
CC	-----	FT	By similarity.
CC	-----	SQ	SEQUENCE 61 AA; 6385 MW;
CC	-----	SQ	B7BF14DCDD28A73D CRC64;
CC	-----	RP	NUCLEOTIDE SEQUENCE.
CC	-----	RC	STRAIN=N=70-15;
CC	-----	RA	Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
CC	-----	RA	Ait-zahra M., Allen T., An P., Anderson M., Anderson S., Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A., Bayul T., Blitskhayen B., Bloom T., Blye J., Boguslavskiy L., Borowsky M., Boukhaler B., Brunaca A., Butler J., Calixte N., Calvo S., Canarata J., Campo K., Chang J., Chesiatsang Y., Citroen M., Collymore A., Considine T., Cook T., Cooke P., Corum B., Cuomo C., David R., Davot T., Dodge S., Dooley K., Dorje P., Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R., Erickson J., Farina A., Faro S., Ferreira P., Fischer H., Gieser D., Galagan J., Gage K., Gerner S., Gneire S., Grandbois B., Graham J., Goettet A., Hall J., Hatcher A., Higgins H., Hagopian D., Hagos B., Horn A., Houde N., Hughes L., Huime W., Husby E., Iliev I., Jaffie D., Jones C., Kamal M., Kamat A., Kamvysellis M., Karlsson E., Keells C., Kleu A., Kiser P., Kodira C., Kulbokas E., Labutti K., Lam D., Landers T., Legre J., Levine S., Liu X., Lokytsaeng T., Lucien O., Lindblad-ton K., Lui A., Ma L.J., Mabbitt J., Macdonald J., Manning J., Marabelli R., Maru K., Mattheus C., Mauceli E., McCarthy M., McDonough S., McGhee T., Melidim J., Menes L., Mesirov J., Mihalev A., Mihova T., Mikkelson T., Mienga V., Moru K., Mores J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C., Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C., Norbu N., O'donnell P., Okawo O., O'leary S., Omotosho B., Parker S., Perzin D., Phunkhang P., Piqani B., Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C., Larsen A.G., Vogensen F.K., Josephsen J.;
CC	-----	Q9BFS5	RESULT 8
CC	-----	Q9BFS5_LACSK PRELIMINARY;	Q9BFS5_LACSK PRELIMINARY;
CC	-----	ID Q9BFS5;	ID Q9BFS5;
CC	-----	AC	AC
CC	-----	DT 10-MAY-2005 (TREMBrel. 30, Created)	DT 10-MAY-2005 (TREMBrel. 30, Last sequence update)
CC	-----	DT 10-MAY-2005 (TREMBrel. 30, Last annotation update)	DT 10-MAY-2005 (TREMBrel. 30, Last annotation update)
CC	-----	DE Sakacin P (SpaPa).	DE Sakacin P (SpaPa).
CC	-----	GN Name=spPa;	GN Name=spPa;
CC	-----	OS Lactobacillus sakei.	OS Lactobacillus sakei.
CC	-----	OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;	OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
CC	-----	OC Lactobacillus.	OC Lactobacillus.
CC	-----	OX NCBI_TaxID=1599;	OX NCBI_TaxID=1599;
CC	-----	RN [1]	RN [1]
CC	-----	RP NUCLEOTIDE SEQUENCE.	RP NUCLEOTIDE SEQUENCE.
CC	-----	RC STRAIN=M1401;	RC STRAIN=M1401;
CC	-----	RX MEDLINE=94012114; PubMed=8407671;	RX MEDLINE=94012114; PubMed=8407671;
CC	-----	RA Larsen A.G., Vogensen F.K., Josephsen J.;	RA Larsen A.G., Vogensen F.K., Josephsen J.;

RA Recta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schubbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
 RA Spencer B., Stalker J., Strange-thomann N., Stearopoulos S.,
 RA Stetson K., Stone C., Stone S., Stubbs M., Talama J., Tchuinga P.,
 RA Tenzing P., Tesfaye S., Theodore J., Thoulouzaeng Y., Topham K.,
 RA Tovey S., Tsamli T., Tsomo N., Vallee D., Vassiliev R.,
 RA Venkataraman V., Vinson J., Wade C., Wang S., Wangchuk T.,
 RA Wang D., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RA "The genome sequence of Magnaporthe grisea.";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
 RL CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 CC Preliminary data.
 DR AACU00014301; EAA48943.1; -; Genomic_DNA.
 KW Hypothetical Protein.
 SQ SEQUENCE 714 AA; 81698 MW; FE74ED11113DCAP3 CRC64;
 Query Match Score 64; DB 2; Length 714;
 Best Local Similarity 34.2%; Pred. No. 29; Indels 0; Gaps 0;
 Matches 13; Conservative 7; Mismatches 18; Indels 0; Gaps 0;
 DR 7 NGVHCTKNSLWGKVRLKMKYDQNTTYMGRLODILGW 44
 DB .. 626 NNVHTCLNSDNGTLFKSSLSDFYQMFGRSDTTIHW 663

RESULT 10
 QBYK80 ANASP ID QBYK80_ ANASP PRELIMINARY; PRT; 590 AA.
 AC QBYK80_ (TREMBLrel. 01-MAR-2002 (TREMBLrel. 01-MAR-2002 (TREMBLrel. 01-JUN-2003 (TREMBLrel. 20 Created) 20 Last sequence update) 24. Last annotation update)
 DR All18037 protein.
 GN OrderedLocusNames=All18037;
 OS Anabaena sp. (strain PCC 7120).
 OC Plasmid pCC7120gamma.
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 NCBI_TaxID=103690;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 MEDLINE=21593285; Pubmed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kimura T.,
 RA Watanabe A., Iriuchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimpio S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RR "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res 8:205-213(2001).
 DR EMBL; AP003603; BAB77367.1; -; Genomic_DNA.
 DR PIR; AF5555; AF2355.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO:0009291; P:unidirectional conjugation; IEA.
 KW Complete proteome; Plasmid.
 SQ SEQUENCE 590 AA; 64333 MW; TECA68DF6FE3BA469 CRC64;

Query Match Score 63; DB 2; Length 590;
 Best Local Similarity 35.3%; Pred. No. 31; Mismatches 23; Indels 2; Gaps 1;
 Matches 18; Conservative 8; Mismatches 23; Indels 2; Gaps 1;

Qy 3 YYGTTGVHCTKNSLWGKVRLKMKYDQNTTYMGRLODILGWATGAFGKTF 53
 ID QBYK80_ FUSNN PRELIMINARY; PRT; 1582 AA.
 AC QBYK80_ (TREMBLrel. 01-JUN-2002 (TREMBLrel. 01-MAR-2004 (TREMBLrel. 21. Last sequence update) 26. Last annotation update)
 DR 01-JUN-2002 (TREMBLrel. 01-MAR-2004 (TREMBLrel. 21. Last sequence update) 26. Last annotation update)
 DB Fusobacterium outer membrane protein family.
 GN OrderedLocusNames=FN1554;
 OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 OC Fusobacterium; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 OC NCBI_TaxID=76856;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=21188639; PubMed=11889109;
 DR DOI=10.1128/JB.184.7.2005-2018.2002;
 RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
 RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltzman B., Bernal A.,
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Forstein M., Kyrides N.C., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 nucleatum strain ATCC 25586";
 RT J. Bacteriol. 184:2005-2018 (2002).
 RL EMBL; AE00951; AAL9360.1; -; Genomic_DNA.
 DR InterPro; IPR005546; Auto_transptbeta.
 DR InterPro; IPR001014; Ribosomal_L23.
 DR Pfam; PF03197; Autotransporter_1.
 DR PROSITE; PS00050; RIBOSOMAL_L23; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 1582 AA; 167889 MW; 666638793A005BB4F CRC64;

Query Match Score 63; DB 2; Length 1582;
 Best Local Similarity 35.2%; Pred. No. 94; Mismatches 6; Indels 8; Gaps 3;
 Matches 19; Conservative 6; Mismatches 21; Indels 8; Gaps 3;

Qy 4 YGTNGVHCTKNSLWGKVRLKMKYDQNTTYMGRLODILGW---GWATGAFGKTF 53
 ID QBYRHH7_ FUSNN PRELIMINARY; PRT; 1630 AA.
 AC QBYRHH7_ (TREMBLrel. 01-JUN-2002 (TREMBLrel. 01-MAR-2004 (TREMBLrel. 21. Last sequence update) 26. Last annotation update)
 DR 01-JUN-2002 (TREMBLrel. 01-MAR-2004 (TREMBLrel. 21. Last sequence update) 26. Last annotation update)
 DB Fusobacterium outer membrane protein family.
 GN OrderedLocusNames=FN20477;
 OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 OC Fusobacterium.
 OC NCBI_TaxID=76856;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=21188639; PubMed=11889109;
 DR DOI=10.1128/JB.184.7.2005-2018.2002;
 RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
 RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltzman B., Bernal A.,
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Forstein M., Kyrides N.C., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium

Best Local Similarity 35.9%; Pred. No. 38;
Matches 14; Conservative 9; Mismatches 7; Indels 9; Gaps 2;
Matches 14;

Qy	5 GTNGVHCTKNSLWGKVRLKMKYDONTTVM--GRLODL 41
: : : : : : : : : : : :	: : : : : : : : : : : :
Db	335 GDDEIIATRNNW-----YEYHRNSTLMNVGRVDVL 366

Search completed: May 2, 2006, 17:30:32
Job time : 237 secs

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OM protein - protein search, using sw model

Run on: May 2, 2006, 17:30:50 ; Search time 46 Seconds
(without alignments)
97.054 Million cell updates/sec

Title: US-10-644-927-1

Perfect score: 304

Sequence: 1 KTYGTTNGVHCTKNSLWGKV.....GRLQDILGNATGAFGKTFH 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 40%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/picodata/1/iaa/5_COMB.pep:
2: /cgn2_6/picodata/1/iaa/6_COMB.pep:
3: /cgn2_6/picodata/1/iaa/H_COMB.pep:
4: /cgn2_6/picodata/1/iaa/PCTUS_COMB.pep:
5: /cgn2_6/picodata/1/iaa/RE_COMB.pep:
6: /cgn2_6/picodata/1/iaa/backfiles1.pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	69.5	22.9	420	2	US-09-328-352-5261	Sequence 5261, AP
2	64	21.1	61	2	US-09-058-507C-5	Sequence 5, Appli
3	62	20.4	85	2	US-09-270-767-44549	Sequence 44549, A
4	60	19.7	36	2	US-08-924-622C-69	Sequence 69, Appli
5	60	19.7	37	2	US-09-030-619-209	Sequence 209, APP
6	60	19.7	37	2	US-09-444-281-90	Sequence 90, Appli
7	60	19.7	61	2	US-08-924-622C-68	Sequence 68, Appli
8	60	19.7	300	2	US-09-932-616-9	Sequence 9, Appli
9	59.5	19.6	577	2	US-09-248-795A-18807	Sequence 18807, A
10	59	19.4	62	2	US-08-924-622C-71	Sequence 71, Appli
11	56.5	18.6	242	2	US-09-543-681A-4928	Sequence 4928, AP
12	56	18.4	66	2	US-09-167-53A-4650	Sequence 4680, AP
13	56	18.4	909	2	US-09-982-616-11	Sequence 11, Appli
14	56	18.4	10182	2	US-09-134-001C-3159	Sequence 3159, Ap
15	55.5	18.3	243	2	US-09-246-295-13	Sequence 13, Appli
16	55.5	18.3	244	2	US-09-632-570-13	Sequence 13, Appli
17	55.5	18.3	244	2	US-09-632-575-43	Sequence 43, Appli
18	55	18.1	41	2	US-08-924-622C-70	Sequence 70, Appli
19	55	18.1	177	2	US-09-248-795A-18821	Sequence 18821, A
20	54.5	17.9	494	2	US-08-378-313-23	Sequence 23, Appli
21	54.5	17.9	494	2	US-08-378-313-29	Sequence 29, Appli
22	54.5	17.9	641	2	US-09-071-035-456	Sequence 456, APP
23	54.5	17.9	641	2	US-10-206-576-456	Sequence 456, APP
24	54.5	17.9	1313	2	US-09-071-035-450	Sequence 450, APP
25	54.5	17.9	1313	2	US-09-071-035-454	Sequence 454, APP
26	54.5	17.9	1313	2	US-10-206-576-450	Sequence 450, APP
27	54.5	17.9	1313	2	US-10-206-576-454	Sequence 454, APP

ALIGNMENTS

RESULT 1
US-09-328-352-5261
; Sequence 5261, Application US/09328352
; Patent No. 6562938
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5261
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-5261

Query Match 22.9% ; Score 69.5; DB 2; Length 420;
Best Local Similarity 38.5%; Pred. No. 0.47%;
Matches 20; Conservative 8; Mismatches 13; Indels 11; Gaps 4;

Qy 1 KTYGTTNGVHCTKNSLWGKV.....GRLQDILGNATGAFGKTFH 44
Db 361 ESVYTNPKSKHSNKRANINTK--NNTPSGDRDDYTTRLRDTTSPLIGW 409

RESULT 2
US-09-068-507C-5
; Sequence 5261, Application US/09068507C
; Patent No. 6730951
; GENERAL INFORMATION:
; APPLICANT: BIJSINK, VINCENT et al.
; TITLE OF INVENTION: HETEROLOGOUS AND HOMOLOGOUS PROTEINS
; FILE REFERENCE: 1380-0122P
; CURRENT APPLICATION NUMBER: US/09/068,507C
; CURRENT FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Lactobacillus sake
; US-09-068-507C-5

Query Match 21.1% ; Score 64; DB 2; Length 61;
Best Local Similarity 36.7%; Pred. No. 0.23%;
Matches 18; Conservative 4; Mismatches 9; Indels 18; Gaps 4;

US-03-030-619-209 Application US/09030619B
; Sequence 209, Application US/09030619B
; Patent No. 6503881
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Briley, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; WITH ANTIBIOTICS
; FILE REFERENCE: 660081-406
; CURRENT APPLICATION NUMBER: US/09/030, 619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 209
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Leuconostoc gelidum
; FEATURE:
; OTHER INFORMATION: xaa means any amino acid
US-09-270-767-44549
; Query Match Score 62; DB 2; Length 85;
; Best Local Similarity 38.2%; Pred. No. 0.66;
; Matches 13; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
Qy 7 NGVATKNSLWGVKLKMKYDONTYMRQLDI 40
Db 46 NACHCNKCSKWSYMMVYIRKYQQGSSSEGVNDI 79

RESULT 4
US-08-924-629C-69
; Sequence 69, Application US/08924629C
; Patent No. 6403082
; GENERAL INFORMATION:
; APPLICANT: Styles, Michael E.
; APPLICANT: Vederas, John C.
; APPLICANT: van Belkum, Marius J.
; APPLICANT: Worobo, Randy W.
; APPLICANT: Worobo, Rodney J.
; APPLICANT: Greer, G. Gordon
; APPLICANT: McMullen, Lynn M.
; APPLICANT: Leisner, Jorgen J.
; APPLICANT: Poor, Alison
; TITLE OF INVENTION: No. 6403082 Bacteriocins, Transport and Vector System and Method
; FILE REFERENCE: 660.1005US
; CURRENT APPLICATION NUMBER: US/08/924, 629C
; CURRENT FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 60/026, 257
; PRIOR FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 69
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Mesenteriocin Y105
US-08-924-629C-69
; Query Match Score 60; DB 2; Length 36;
; Best Local Similarity 48.4%; Pred. No. 0.42;
; Matches 15; Conservative 2; Mismatches 4; Indels 10; Gaps 3;
Qy 3 YYGTNGVHCTKNSL---WGVY-----RLKN 24
Db 2 YYG-NGVHCTKSGCSVNWGEAASAGIHLAN 31

RESULT 5
US-08-924-629C-68
; Sequence 68, Application US/08924629C
; Patent No. 6403082
; GENERAL INFORMATION:
; APPLICANT: Stiles, Michael E.
; APPLICANT: Vederas, John C.
; APPLICANT: van Belkum, Marius J.
; APPLICANT: Worobo, Randy W.
; APPLICANT: Worobo, Rodney J.
; APPLICANT: Green, G. Gordon
; APPLICANT: Mesenteriocin Y105
US-08-924-629C-69
; Query Match Score 60; DB 2; Length 37;
; Best Local Similarity 48.4%; Pred. No. 0.44;
; Matches 15; Conservative 2; Mismatches 4; Indels 10; Gaps 3;
Qy 3 YYGTNGVHCTKNSL---WGVY-----RLKN 24
Db 2 YYG-NGVHCTKSGCSVNWGEAASAGIHLAN 31

RESULT 6
US-09-444-281-90
; Sequence 90, Application US/09444281
; Patent No. 6946261
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Barteld, Daniel
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING
; ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS
; FILE REFERENCE: 660081-411
; CURRENT APPLICATION NUMBER: US/09/444, 281
; CURRENT FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 90
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Leuconostoc gelidum
US-09-444-281-90
; Query Match Score 60; DB 2; Length 37;
; Best Local Similarity 48.4%; Pred. No. 0.44;
; Matches 15; Conservative 2; Mismatches 4; Indels 10; Gaps 3;
Qy 3 YYGTNGVHCTKNSL---WGVY-----RLKN 24
Db 2 YYG-NGVHCTKSGCSVNWGEAASAGIHLAN 31

RESULT 7
US-08-924-629C-68
; Sequence 68, Application US/08924629C
; Patent No. 6403082
; GENERAL INFORMATION:
; APPLICANT: Stiles, Michael E.
; APPLICANT: Vederas, John C.
; APPLICANT: van Belkum, Marius J.
; APPLICANT: Worobo, Randy W.
; APPLICANT: Worobo, Rodney J.
; APPLICANT: Green, G. Gordon
; APPLICANT: Mesenteriocin Y105
US-08-924-629C-69
; Query Match Score 60; DB 2; Length 37;
; Best Local Similarity 48.4%; Pred. No. 0.44;
; Matches 15; Conservative 2; Mismatches 4; Indels 10; Gaps 3;

APPLICANT: McMullen, Lynn M.
 APPLICANT: Leisner, Jorgen J.
 APPLICANT: Poon, Alison
 APPLICANT: Franz, Charles M.A.P.
 TITLE OF INVENTION: No. 6403082elBacteriocins, Transport and Vector System and Method
 CURRENT APPLICATION NUMBER: US/08/924,629C
 CURRENT FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: US 60/005US
 PRIOR FILING DATE: 1996-09-05
 NUMBER OF SEQ ID NOS: 80
 SEQ ID NO: 68
 LENGTH: 61
 TYPE: PRT
 ORGANISM: Leucocin A
 US-08-924-629C-68

RESULT 8
 Query Match 19.7%; Score 60; DB 2; Length 61;
 Best Local Similarity 48.4%; Pred. No. 0.82;
 Matches 15; Conservative 2; Mismatches 4; Indels 10; Gaps 3;

Qy 3 YYGTNGVHCTKNSL---WGVY-----RLKN 24
 Db 26 YYG-NGVHCTKSGCSYNWGEAESAGVHLAN 55

GENERAL INFORMATION:
 APPLICANT: Frances E. Lund
 APPLICANT: Troy D. Randall
 APPLICANT: Santiago Partida-Sanchez
 TITLE OF INVENTION: CD38 MODULATED CHEMOTAXIS
 FILE REFERENCE: AP33438 068443.0106
 CURRENT APPLICATION NUMBER: US/09/982,616
 CURRENT FILING DATE: 2001-10-17
 PRIOR APPLICATION NUMBER: 60/241,065
 PRIOR FILING DATE: 2000-10-17
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 9
 LENGTH: 300
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-982-16-9

RESULT 9
 Query Match 19.7%; Score 60; DB 2; Length 300;
 Best Local Similarity 35.0%; Pred. No. 6.1;
 Matches 14; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 5 GINGVHCTKNSLWGVKVRKKNKYDQNTTYMGRQLDILLGW 44
 Db 113 GTOVPCPKILWWSRKLQHQFTQVQRDMFTELEDTIGY 152

GENERAL INFORMATION:
 APPLICANT: Keith Weinstock et al
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 FILE REFERENCE: 10/196,132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/096,409
 PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO: 18807
 LENGTH: 577
 TYPE: PRT
 ORGANISM: Candida albicans
 US-09-248-796A-18807

Query Match 19.6%; Score 59.5; DB 2; Length 577;
 Best Local Similarity 30.6%; Pred. No. 16;
 Matches 15; Conservative 7; Mismatches 12; Indels 15; Gaps 2;

Qy 6 TNGVHCTKNSLWGVKVRKKNKYDQNTTYMGRQLDILLGWATGAFKTFH 54
 Db 261 TTGVCQDESTLWKL-IPNLKHLANN-----QTSATGKFH 294

RESULT 10
 Query Match 19.6%; Score 59.5; DB 2; Length 577;
 Best Local Similarity 30.6%; Pred. No. 16;
 Matches 15; Conservative 7; Mismatches 12; Indels 15; Gaps 2;

Qy 6 TNGVHCTKNSLWGVKVRKKNKYDQNTTYMGRQLDILLGWATGAFKTFH 54
 Db 261 TTGVCQDESTLWKL-IPNLKHLANN-----QTSATGKFH 294

GENERAL INFORMATION:
 APPLICANT: Stiles, Michael E.
 APPLICANT: Vederas, John C.
 APPLICANT: van Belkum, Marius J.
 APPLICANT: Worobo, Randy W.
 APPLICANT: Greer, G. Gordon
 APPLICANT: McMullen, Lynn M.
 APPLICANT: Leisner, Jorgen J.
 APPLICANT: Poon, Alison
 APPLICANT: Franz, Charles M.A.P.
 TITLE OF INVENTION: No. 6403082elBacteriocins, Transport and Vector System and Method
 FILE REFERENCE: 660_0005US
 CURRENT APPLICATION NUMBER: US/08/924,629C
 CURRENT FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: US 60/026,257
 PRIOR FILING DATE: 1996-09-05
 NUMBER OF SEQ ID NOS: 80
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 71
 LENGTH: 62
 TYPE: PRT
 ORGANISM: Pediocin PA1
 US-08-924-629C-71

Query Match 19.4%; Score 59; DB 2; Length 62;
 Best Local Similarity 37.5%; Pred. No. 1.1;
 Matches 18; Conservative 5; Mismatches 9; Indels 16; Gaps 4;

Qy 3 YYGTNGVHCTKNSL---WGVYRLKNKYDQNTTYMGRQLDILLGWATG 47
 Db 20 YYG-NGVHCTKNSL---WGVYRLKNKYDQNTTYMGRQLDILLGWATG 47

RESULT 11
 Query Match 19.4%; Score 59; DB 2; Length 62;
 Best Local Similarity 37.5%; Pred. No. 1.1;
 Matches 18; Conservative 5; Mismatches 9; Indels 16; Gaps 4;

Qy 3 YYGTNGVHCTKNSL---WGVYRLKNKYDQNTTYMGRQLDILLGWATG 47
 Db 20 YYG-NGVHCTKNSL---WGVYRLKNKYDQNTTYMGRQLDILLGWATG 47

GENERAL INFORMATION:
 APPLICANT: GARY BRETON
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 FILE REFERENCE: 2709-1002-001
 CURRENT APPLICATION NUMBER: US/09/543,681A
 CURRENT FILING DATE: 2000-04-05
 PRIOR APPLICATION NUMBER: US 60/128,706
 PRIOR FILING DATE: 1999-04-09
 NUMBER OF SEQ ID NOS: 8344
 SEQ ID NO: 4928
 LENGTH: 242
 TYPE: PRT
 ORGANISM: Proteus mirabilis
 FEATURE:

NAME/KEY: UNSURE
 LOCATION: (18)
 OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
 US-09-543-681A-4928

Query Match Score 56 %; DB 2; Length 242;
 Best Local Similarity 28.1%; Pred. No. 14; Gaps 3;
 Matches 18; Conservative 8; Mismatches 21; Indels 17;

Qy 4 YGTNGVHCTKNSLWGRVKRILN-----MKYDQNTTYMGRILQDILIGWATEAF 49
 Db 106 YKTSSDTSAKISVEGLVNARNTEOIGGYTIDVTDIKVNDKRAYLGRVADKI--W-TGSS 162

Qy 50 GKT^F 53
 Db 163 ATIF 166

RESULT 12
 US-09-107-532A-4680
 Sequence 4680, Application US/09107532A
 Patent No. 65832/5
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO
 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02454
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Ariello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 4680:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 66 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1...66
 SEQUENCE DESCRIPTION: SEQ ID NO: 4680:

Qy 3 YYGTNGVHCTKNSL---WGK 19
 Db 26 YTG-NGVHCTKNSLWGRVKRILN-----

RESULT 13
 US-09-582-616-11
 ; Sequence 11, Application US/09982616
 ; Patent No. 695584
 ; GENERAL INFORMATION:
 ; APPLICANT: Frances E. Lund
 ; TROY D. Randal
 ; APPLICANT: Santiazo Partida-Sanchez
 ; TITLE OF INVENTION: CDP38 MODULATED CHEMOTAXIS
 ; FILE REFERENCE: AF33438 06843.01.06
 ; CURRENT APPLICATION NUMBER: US/09/982,616
 ; CURRENT FILING DATE: 2001-10-17
 ; PRIOR APPLICATION NUMBER: 60/241,065
 ; PRIOR FILING DATE: 2000-10-17
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 11
 ; LENGTH: 909
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Reverse translation of SM38
 ; US-09-582-616-11

Query Match Score 56 %; DB 2; Length 909;
 Best Local Similarity 32.7%; Pred. No. 85;
 Matches 16; Conservative 2; Mismatches 15; Indels 16; Gaps 2;

Qy 4 YGTNGVHCTKNSLWGRVKRILN-----MKYDQNTTYMGRILQDILIGWATEAF 50
 Db 477 YGTNGTNCA-----YGCNTTYYTGCCARSNGCNWSNGCNG 511

RESULT 14
 US-09-134-001C-3159
 ; Sequence 3159, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 3159
 ; LENGTH: 10182
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 ; US-09-134-001C-3159

Query Match Score 56 %; DB 2; Length 10182;
 Best Local Similarity 46.7%; Pred. No. 1.3e+03;
 Matches 14; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

Qy 6 TNGVHCTKNSLWGRVKRILN-----MKYDQNTTYMGRILQDILIGWATEAF 35
 Db 4753 TQRVNTTRNDLNQNDKLAERKDANTTIDG 4782

RESULT 15
 US-09-216-295-13
 ; Sequence 13, Application US/09216295
 ; Patent No. 6268328

Query Match Score 56 %; DB 2; Length 66;
 Best Local Similarity 60.0%; Pred. No. 3.1.; Mismatches 3; Indels 4; Gaps 2;
 Matches 12; Conservative 1; Sequence Description: SEQ ID NO: 4680:

; GENERAL INFORMATION:
; APPLICANT: Hutchinson, Colin
; Wendl, Dan J.
; TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 13
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Fusarium javanicum (1)
; ORGANISM: Fusarium javanicum (1)
US-09-216-295-13

Query Match 18.3%; Score 55.5; DB 2; Length 243;
Best Local Similarity 31.4%; Pred. No. 19;
Matches 16; Conservative 8; Mismatches 20; Indels 7; Gaps 2;
Qy 6 TNGVHCTKNSIwgkvrLKNMKYDONTTymgrLQDILGNA----TGARGK 51
Db 34 TAGAVTIYNNLwgkDNAES -GEOQCTTNSGEQSDGSIANSVIEWSWTGGQQ 82

Search completed: May 2, 2006, 17:32:07
Job time : 47 secs

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OM protein - protein search, using sw model

Run on: May 2, 2006, 17:42:01 ; Search time 164 Seconds
 (without alignments)
 137.578 Million cell updates/sec

Title: US-10-644-927-1

Perfect score: 304

Sequence: 1 KTYGTNGVHCTKNSLWGKV.....GRLQDILLGWTARGKTPH 54

Scoring table: BLOSUM62

Gapext: Gap 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:
 1: /cgns_6/prodata/1/pubpaas/US07_PUBCOMB.pep:
 2: /cgns_6/prodata/1/pubpaas/US08_PUBCOMB.pep:
 3: /cgns_6/prodata/1/pubpaas/US10A_PUBCOMB.pep:
 4: /cgns_6/prodata/1/pubpaas/US10A_PUBCOMB.pep:
 5: /cgns_6/prodata/1/pubpaas/US10B_PUBCOMB.pep:
 6: /cgns_6/prodata/1/pubpaas/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	304	100.0	54	US-10-544-927-1	Sequence 1, Appli
2	62.0	20.6	558	US-10-781-979-27	Sequence 27, Appli
3	60	19.7	36	US-09-883-333A-69	Sequence 69, Appli
4	60	19.7	37	US-09-930-619-209	Sequence 209, Appli
5	60	19.7	37	US-09-942-609-97	Sequence 97, Appli
6	60	19.7	37	US-10-277-232-209	Sequence 209, Appli
7	60	19.7	37	US-10-277-233-209	Sequence 209, Appli
8	60	19.7	61	US-09-883-343A-68	Sequence 68, Appli
9	60	19.7	300	US-09-982-616-9	Sequence 9, Appli
10	60	19.7	300	US-09-973-307B-2	Sequence 2, Appli
11	60	19.7	300	US-10-495-127-1348	Sequence 1348, Appli
12	60	19.7	300	US-10-454-238-2	Sequence 2, Appli
13	60	19.7	300	US-10-322-696-162	Sequence 162, Appli
14	60	19.7	300	US-10-253-267-34	Sequence 34, Appli
15	60	19.7	688	US-10-450-763-37242	Sequence 37242, A
16	59	19.4	62	US-09-883-343A-71	Sequence 71, Appli
17	59	19.4	399	US-10-359-493-6141	Sequence 6141, Appli
18	59	19.4	753	US-10-983-198-42	Sequence 42, Appli
19	58.5	19.2	95	US-10-422-599-280304	Sequence 280304,
20	58	19.1	511	US-10-424-599-213009	Sequence 213009,
21	57.5	18.9	461	US-10-410-432-10	Sequence 10, Appli
22	57.5	18.9	461	US-10-663-174-10	Sequence 10, Appli
23	57.5	18.9	461	US-10-984-956-10	Sequence 10, Appli
24	57.5	18.9	461	US-10-732-923-1935	Sequence 1935, A
25	57.5	18.9	643	US-11-097-143-40056	Sequence 40056, A
26	57	18.8	564	US-10-424-599-19752	Sequence 19752,
27	57	18.8	581	US-10-282-122A-72532	Sequence 72532, A

RESULT 1
 US-10-644-927-1
 Sequence 1, Application US10644927
 Publication No. US20050153881A1

GENERAL INFORMATION:

- APPLICANT: Stern, Norman J.
- APPLICANT: Svetoch, Edward A.
- APPLICANT: Erublanov, Boris V.
- APPLICANT: Voldina, Larisa I.
- APPLICANT: Kovalev, Yuri N.
- APPLICANT: Kudryavtseva, Tamara Y.
- APPLICANT: Perlygin, Vladimir V.
- APPLICANT: Pokhilenco, Victor D.
- APPLICANT: Levchuk, Vladimir P.
- APPLICANT: Borenkova, Valery N.
- APPLICANT: Svetoch, Olga E.
- APPLICANT: Mitevich, Eugene V.
- APPLICANT: Mitevich, Irina P.

TITLE OF INVENTION: Bacteriocins and Novel Bacterial Strains

FILE REFERENCE: D.N. 0135_03

CURRENT APPLICATION NUMBER: US/10/644,927

CURRENT FILING DATE: 2005-08-21

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1

LENGTH: 54

TYPE: PRT

ORGANISM: Lactobacillus salivarius

US-10-644-927-1

Query Match 100.0%; **Score** 304; **DB 5;** Length 54;
Best Local Similarity 100.0%; **Pred. No.** 1..4e-31; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Matches 54; **Conservative** 0;

Qy 1 KTYGTNGVHCTKNSLWGKVRLKNNKYDQNTTYYMGRQLDILGWATGAFGKTFH 54

Ds 1 KTYGTNGVHCTKNSLWGKVRLKNNKYDQNTTYYMGRQLDILGWATGAFGKTFH 54

RESULT 2
 US-10-781-979-27
 Sequence 27, Application US10781979
 Publication No. US20040250311A1

GENERAL INFORMATION:

- APPLICANT: Carozzi, Nadine
- APPLICANT: Haroiss, Tracy
- APPLICANT: Koziel, Michael G.
- APPLICANT: Duck, Nicholas B.
- APPLICANT: Carr, Brian

TITLE OF INVENTION: ARMI-008, A Delta-Endotoxin Gene and

TITLE OF INVENTION: Methods for its Use
 FILE REFERENCE: 045600/274147
 CURRENT APPLICATION NUMBER: US 10/781,979
 CURRENT FILING DATE: 2004-02-20
 PRIOR APPLICATION NUMBER: 60/448,797
 PRIOR FILING DATE: 2003-02-20
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 27
 LENGTH: 558
 TYPE: PRT
 ORGANISM: *Bacillus thuringiensis*
 US-10-781-979-27

Query Match 20.6%; Score 62.5; DB 5; Length 558;
 Best Local Similarity 27.7%; Pred. No. 32;
 Matches 13; Conservative 8; Mismatches 17; Indels 9;
 Gaps 2;

Qy : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 26 IECMSNEHSSKREEMMLWDVQRQKLSWSRNLLYNGDFEDVSNGWKT 72

RESULT 3

US-09-883-343A-69

Sequence 69, Application US/09883343A
 Publication No. US2003039632A1
 GENERAL INFORMATION:
 APPLICANT: Stiles, Michael E.
 APPLICANT: Vederas, John C.
 APPLICANT: van Belkum, Marius J.
 APPLICANT: Worobo, Randy W.
 APPLICANT: Greer, G. Gordon
 APPLICANT: McMullen, Lynn M.
 APPLICANT: Leisner, Jorgen J.
 APPLICANT: Poon, Aljeion
 APPLICANT: Franz, Charles M.A.P.
 TITLE OF INVENTION: NO. US2003039632A1 Bacteriocins, Transport and Vector System and Method of Use Thereof
 FILE REFERENCE: 660.0005US
 CURRENT APPLICATION NUMBER: US/09/883,343A
 CURRENT FILING DATE: 2001-06-19
 PRIOR APPLICATION NUMBER: US/08/924,629
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: US 60/026,257
 PRIOR FILING DATE: 1996-09-05
 NUMBER OF SEQ ID NOS: 80
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 69
 LENGTH: 36
 TYPE: PRT
 ORGANISM: Mesenteriocin Y105
 US-09-883-343A-69

Query Match 19.7%; Score 60; DB 3; Length 36;
 Best Local Similarity 48.4%; Pred. No. 3;
 Matches 15; Conservative 2; Mismatches 4; Indels 10; Gaps 3;

Qy : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 3 YYGTNGVHCTKNSL--WGKV----RLKN 24
 Db 2 YYG-NGVHCTKSGCSVNVGEAFSAGVHLAN 31

RESULT 4

US-09-030-619-209

Sequence 209, Application US/09030619B
 Patent No. US2003035031A1
 GENERAL INFORMATION:
 APPLICANT: Krieger, Timothy J.
 APPLICANT: Taylor, Robert
 APPLICANT: Erfile, Douglass
 APPLICANT: Fraser, Janet R.
 APPLICANT: West, Michael H.P.
 APPLICANT: McNicol, Patricia J.
 APPLICANT: Title of Invention: Compositions and Methods for Treating

APPLICANT: McNicol, Patricia J.
 TITLE OF INVENTION: Compositions and Methods for Treating Infections Using Cationic Peptides Alone or in Combination
 TITLE OF INVENTION: With Antibiotics
 FILE REFERENCE: 660081.406
 CURRENT APPLICATION NUMBER: US/09/030,619B
 CURRENT FILING DATE: 1998-02-25
 NUMBER OF SEQ ID NOS: 232
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 209
 LENGTH: 37
 TYPE: PRT
 ORGANISM: Leuconostoc gelidum
 US-09-030-619-209

Query Match 19.7%; Score 60; DB 3; Length 37;
 Best Local Similarity 48.4%; Pred. No. 3.1;
 Matches 15; Conservative 2; Mismatches 4; Indels 10; Gaps 3;

Qy : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 3 YYGTNGVHCTKNSL--WGKV----RLKN 24
 Db 2 YYG-NGVHCTKSGCSVNVGEAFSAGVHLAN 31

RESULT 5

US-09-912-609-97

Sequence 97, Application US/0912609
 Publication No. US20020041898A1
 GENERAL INFORMATION:
 APPLICANT: Unger, Evan C.
 APPLICANT: Matsunaga, Terry Onichi
 APPLICANT: Ramaswami, Varadarajan
 APPLICANT: Ronanowski, Marek J.
 TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
 FILE REFERENCE: 5030-0001-24
 CURRENT APPLICATION NUMBER: US/09/912,609
 CURRENT FILING DATE: 2001-07-25
 PRIOR APPLICATION NUMBER: 09/703,474
 PRIOR FILING DATE: 2000-10-31
 PRIOR APPLICATION NUMBER: 09/478,124
 PRIOR FILING DATE: 2000-01-05
 NUMBER OF SEQ ID NOS: 131
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 97
 LENGTH: 37
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: peptide
 US-09-912-609-97

Query Match 19.7%; Score 60; DB 3; Length 37;
 Best Local Similarity 48.4%; Pred. No. 3.1;
 Matches 15; Conservative 2; Mismatches 4; Indels 10; Gaps 3;

Qy : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 3 YYGTNGVHCTKNSL--WGKV----RLKN 24
 Db 2 YYG-NGVHCTKSGCSVNVGEAFSAGVHLAN 31

RESULT 6

US-10-277-232-209

Sequence 209, Application US/10277232
 Publication No. US20030211537A1
 GENERAL INFORMATION:
 APPLICANT: Krueger, Timothy J.
 APPLICANT: Taylor, Robert
 APPLICANT: Erfile, Douglass
 APPLICANT: Fraser, Janet R.
 APPLICANT: West, Michael H.P.
 APPLICANT: McNicol, Patricia J.
 APPLICANT: Title of Invention: Compositions and Methods for Treating

TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION WITH ANTIBIOTICS
 TITLE OF INVENTION: WITH ANTIBIOTICS
 FILE REFERENCE: 660081_406C1
 CURRENT APPLICATION NUMBER: US/10/277,232
 CURRENT FILING DATE: 2002-11-27
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 209
 LENGTH: 37
 TYPE: PRT
 ORGANISM: Leuconostoc gelidum
 US-10-277-232-209

Query Match 19.7%; Score 60; DB 4; Length 37;
 Best Local Similarity 48.4%; Pred. No. 3.1;
 Matches 15; Conservative 2; Mismatches 4; Indels 10; Gaps 3;
 Qy 3 YYGTNGVHCTKNSL---WKGKV-----RLKN 24
 Db 2 YYG-NGVHCTKSGCSVNWGEAFSAGVHLAN 31

RESULT 7

US-10-277-233-209
 Sequence 209, Application US/10277233
 Publication No. US20030232250A1
 GENERAL INFORMATION:
 APPLICANT: Krieger, Timothy J.
 APPLICANT: Taylor, Robert
 APPLICANT: Erlie, Douglas
 APPLICANT: Fraser, Janet R.
 APPLICANT: West, Michael H.P.
 APPLICANT: McNicol, Patricia J.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
 TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
 TITLE OF INVENTION: WITH ANTIBIOTICS
 FILE REFERENCE: 660081_406CL
 CURRENT APPLICATION NUMBER: US/10/277,233
 CURRENT FILING DATE: 2002-10-18
 NUMBER OF SEQ ID NOS: 232
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 209
 LENGTH: 37
 TYPE: PRT
 ORGANISM: Leuconostoc gelidum
 US-10-277-233-209

Query Match 19.7%; Score 60; DB 4; Length 37;
 Best Local Similarity 48.4%; Pred. No. 3.1;
 Matches 15; Conservative 2; Mismatches 4; Indels 10; Gaps 3;
 Qy 3 YYGTNGVHCTKNSL---WKGKV-----RLKN 24
 Db 2 YYG-NGVHCTKSGCSVNWGEAFSAGVHLAN 31

RESULT 8

US-09-883-343A-68
 Sequence 68, Application US/09883343A
 Publication No. US2003039632A1
 GENERAL INFORMATION:
 APPLICANT: Stiles, Michael E.
 APPLICANT: Veders, John C.
 APPLICANT: van Belkum, Marius J.
 APPLICANT: Worobo, Randy W.
 APPLICANT: Worobo, Rooney J.
 APPLICANT: Greer, G. Gordon
 APPLICANT: McMullen, Lynn M.
 APPLICANT: Leisner, Jorgen J.
 APPLICANT: Poon, Alison
 APPLICANT: Franz, Charles M.A.P.
 TITLE OF INVENTION: No. US2003039632A1elBacteriocins, Transport and Vector System and
 FILE REFERENCE: 660_0005US

CURRENT APPLICATION NUMBER: US/09/883-343A
 CURRENT FILING DATE: 2001-06-19
 PRIOR APPLICATION NUMBER: US/08/924,629
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: US 60/026,257
 PRIOR FILING DATE: 1996-09-05
 NUMBER OF SEQ ID NOS: 80
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 68
 LENGTH: 61
 TYPE: PRT
 ORGANISM: Leucococcin A
 US-09-883-343A-68

Query Match 19.7%; Score 60; DB 3; Length 61;
 Best Local Similarity 48.4%; Pred. No. 5.5;
 Matches 15; Conservative 2; Mismatches 4; Indels 10; Gaps 3;

Qy 3 YYGTNGVHCTKNSL---WKGKV-----RLKN 24
 Db 26 YYG-NGVHCTKSGCSVNGEAEASAGVHLAN 55

RESULT 9

US-09-982-616-9
 Sequence 9, Application US/09982616
 Publication No. US20020127646A1
 GENERAL INFORMATION:
 APPLICANT: Frances E. Lund
 APPLICANT: Troy D. Randall
 APPLICANT: Santiago Partida-Sanchez
 TITLE OF INVENTION: CD38 MODULATED CHEMOTAXIS
 FILE REFERENCE: AP31438 068443_0106
 CURRENT APPLICATION NUMBER: US/09/982,616
 CURRENT FILING DATE: 2001-10-17
 PRIOR APPLICATION NUMBER: 60/241,065
 PRIOR FILING DATE: 2000-10-17
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 9
 LENGTH: 300
 TYPE: PRT
 ORGANISM: Homo sapien
 US-09-982-616-9

Query Match 19.7%; Score 60; DB 3; Length 300;
 Best Local Similarity 35.0%; Pred. No. 3.3;
 Matches 14; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 5 GTNGVHCTKNSLWKGVRKNNKYDNTYMGRLQDLLGW 44
 Db 113 GTQTVPCNKILLWSRIKDLAHQFTQVQRDMFTLEBLLGY 152

RESULT 10

US-09-773-307B-2
 Sequence 2, Application US/09773307B
 Publication No. US2003027134A1
 GENERAL INFORMATION:
 APPLICANT: BML, INC.
 TITLE OF INVENTION: Method of Detecting Risk Factor for Onset of Diabetes
 FILE REFERENCE: PBM37
 CURRENT APPLICATION NUMBER: US/09/773,307B
 CURRENT FILING DATE: 2001-01-31
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 2
 LENGTH: 300
 TYPE: PRT
 ORGANISM: Hominiidae
 US-09-773-307B-2

Query Match 19.7%; Score 60; DB 3; Length 300;

Best Local Similarity 35.0%; Pred. No. 33; Matches 14; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 5 GTNGVHCTKNSLWGVRLKMKYDNTTYNGRLQDILLGW 44
Db 113 GTQTPCNKILLWSRKDLAHQFTQVQRDMFTLEDILGY 152

RESULT 11
US-10-295-027-1348
; Sequence 1348, Application US/10295027
; Publication No. US20010232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Azziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezsi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Bos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; Title of Invention: Methods of Screening For Modulators of Cancer
; FILE REFERENCE: 018511-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-9
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1348
; LENGTH: 300

Qy 5 GTNGVHCTKNSLWGVRLKMKYDNTTYNGRLQDILLGW 44
Db 113 GTQTPCNKILLWSRKDLAHQFTQVQRDMFTLEDILGY 152

RESULT 12
US-10-454-238-2
; Sequence 1348, Application US/10454238
; Publication No. US20030604
; CURRENT FILING DATE: 2003-06-04
; PRIORITY APPLICATION NUMBER: US 09/773,307
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Hominidae

Qy 5 GTNGVHCTKNSLWGVRLKMKYDNTTYNGRLQDILLGW 44
Db 113 GTQTPCNKILLWSRKDLAHQFTQVQRDMFTLEDILGY 152

RESULT 13
US-10-322-696-162
; Sequence 162, Application US/10322696
; Publication No. US20040166190A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 529452001200
; CURRENT APPLICATION NUMBER: US/10/322,696
; CURRENT FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 162
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens

Qy 5 GTNGVHCTKNSLWGVRLKMKYDNTTYNGRLQDILLGW 44
Db 113 GTQTPCNKILLWSRKDLAHQFTQVQRDMFTLEDILGY 152

RESULT 14
US-10-753-267-34
; Sequence 34, Application US/10753267
; Publication No. US2005037946A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stagliano, Nancy E.
; APPLICANT: Actor, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Doneghe, Mary A.
; APPLICANT: Rodriguez-Way, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6165, 10102, 21061, 57,
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8935, 8701,
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 337,
; TITLE OF INVENTION: 9380, 9695, 41671, 32612, 10571, 41143, 19319, 43696, 8921, 8993, 955,
; TITLE OF INVENTION: 4450, 41922, 2552, 2417, 19319, 43696, 8921, 8993, 955,
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 54, 16408
; TITLE OF INVENTION: 4228, 11201, 13886, 13942, 1673, 54946 OR 2419

Qy 5 GTNGVHCTKNSLWGVRLKMKYDNTTYNGRLQDILLGW 44
Db 113 GTQTPCNKILLWSRKDLAHQFTQVQRDMFTLEDILGY 152

CURRENT APPLICATION NUMBER: US/10/753,267
 CURRENT FILING DATE: 2004-01-08
 PRIOR FILING DATE: 2003-01-13
 PRIOR APPLICATION NUMBER: US 65/439,683
 PRIOR FILING DATE: 2003-02-05
 PRIOR APPLICATION NUMBER: US 60/445,216
 PRIOR FILING DATE: 2003-02-18
 PRIOR APPLICATION NUMBER: US 60/454,189
 PRIOR FILING DATE: 2003-03-12
 PRIOR APPLICATION NUMBER: US 60/457,541
 PRIOR FILING DATE: 2003-03-25
 PRIOR APPLICATION NUMBER: US 60/466,411
 PRIOR FILING DATE: 2003-04-29
 PRIOR APPLICATION NUMBER: US 60/469,041
 PRIOR FILING DATE: 2003-05-08
 PRIOR APPLICATION NUMBER: US 60/477,414
 PRIOR FILING DATE: 2003-06-10
 PRIOR APPLICATION NUMBER: US 60/478,560
 PRIOR FILING DATE: 2003-06-13
 PRIOR FILING DATE: 2003-07-24
 PRIOR FILING NUMBER: US 60/489,772
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 130
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 34
 LENGTH: 300
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-753-267-34

Query Match 19.7%; Score 60; DB 5; Length 300;
 Best Local Similarity 35.0%; Pred. No. 33; Indels 0;
 Matches 14; Conservative 7; Mismatches 19; Gaps 0;
 Qy 5 GTNGVACTNSLNGKVRKKNKYDQNTTYMGRQLQDILGW 44
 Db 113 GTQTPCNKILWSRKIDLAHQFTQYQDMFTLEDILGY 152

RESULT 15

US-10-450-763-37242
 Sequence 37242, Application US/10450763
 Publication No. US20050196734A1
 GENERAL INFORMATION:
 APPLICANT: Hyseq, Inc
 TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
 FILE REFERENCE: 790C1P/US
 CURRENT APPLICATION NUMBER: US/10/450,763
 CURRENT FILING DATE: 2003-06-11
 PRIOR FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: 09/540,217
 PRIOR FILING DATE: 2000-03-31
 PRIOR APPLICATION NUMBER: 09/649,167
 PRIOR FILING DATE: 2000-08-23
 NUMBER OF SEQ ID NOS: 60736
 SOFTWARE: Custom
 SEQ ID NO 37242
 LENGTH: 688
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: DOMAIN
 LOCATION: (49)-(136)
 OTHER INFORMATION: ADP-ribosyl cyclase domain identified by PFam, accession name
 OTHER INFORMATION: Rib_hydrolyse, E-value=1.e-68, PFam score of 219.7
 US-10-450-763-37242

Query Match 19.7%; Score 60; DB 5; Length 688;
 Best Local Similarity 35.0%; Pred. No. 85; Indels 0; Gaps 0;
 Matches 14; Conservative 7; Mismatches 19; Gaps 0;

5 GTNGVACTNSLNGKVRKKNKYDQNTTYMGRQLQDILGW 44
 83 GTQTPCNKILWSRKIDLAHQFTQYQDMFTLEDILGY 152

Search completed: May 2, 2006, 17:45:42
 Job time : 165 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 17:43:06 ; Search time 25 Seconds
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Title: BLOSUM62 Scoring table: Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Applications AA_New:
 1: /SIDSS/ptodata/2/pubpa/us08_NBW_PUB.pep1:
 2: /SIDSS/ptodata/2/pubpa/us06_NBW_PUB.pep1:
 3: /SIDSS/ptodata/2/pubpa/us07_NBW_PUB.pep1:
 4: /SIDSS/ptodata/2/pubpa/us08_NBW_PUB.pep1:
 5: /SIDSS/ptodata/2/pubpa/BCT_NEW_PUB.pep1:
 6: /SIDSS/ptodata/2/pubpa/US05_NEW_PUB.pep1:
 7: /SIDSS/ptodata/2/pubpa/us09_NBW_PUB.pep1:
 8: /SIDSS/ptodata/2/pubpa/us10_NBW_PUB.pep1:
 9: /SIDSS/ptodata/2/pubpa/us10_NEW_PUB.pep1:
 10: /SIDSS/ptodata/2/pubpa/us11_NBW_PUB.pep1:
 11: /SIDSS/ptodata/2/pubpa/us11_NBW_PUB.pep1:
 12: /SIDSS/ptodata/2/pubpa/us60_NBW_PUB.pep1:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	21.7	557	11 US-11-188-258-21798	Sequence 21798, A
2	65.5	21.5	471	11 US-11-188-298-21598	Sequence 21598, A
3	62.5	20.6	446	11 US-11-188-298-13174	Sequence 13174, A
4	60	19.7	37	11 US-11-088-783-90	Sequence 90, APP
5	60	19.7	300	11 US-11-059-924-7	Sequence 7, APP
6	57.5	18.9	670	11 US-11-188-298-18003	Sequence 18003, A
7	56.5	18.8	473	11 US-11-188-298-15548	Sequence 15548, A
8	56.5	18.6	812	11 US-11-188-298-9586	Sequence 9586, AP
9	56	18.4	147	11 US-11-188-298-13016	Sequence 13006, A
10	55.5	18.3	226	11 US-11-188-298-15017	Sequence 15017, A
11	54.5	17.9	480	9 US-10-915-002-299	Sequence 299, APP
12	53.5	17.6	56	9 US-10-922-415-3	Sequence 3, APP
13	53.5	17.6	134	9 US-10-922-415-4	Sequence 4, APP
14	53.5	17.6	278	11 US-11-087-089-587	Sequence 587, APP
15	53.5	17.6	353	11 US-11-087-093-5419	Sequence 5419, APP
16	53.5	17.6	364	11 US-11-087-093-3112	Sequence 3112, APP
17	53.5	17.6	373	11 US-11-087-093-7159	Sequence 7159, APP
18	53.5	17.6	510	11 US-11-188-298-394	Sequence 394, APP
19	53.5	17.6	510	11 US-11-188-298-6950	Sequence 6950, APP
20	53.5	17.6	510	11 US-11-188-212158	Sequence 21258, APP
21	53.5	17.6	663	11 US-11-188-298-21626	Sequence 21626, APP

ALIGNMENTS

RESULT 1
 US-11-188-298-21798 ; Sequence 21798, Application US/11188298 ; Publication No. US20060075522A1

/ GENERAL INFORMATION:
 / APPLICANT: Abad, Mark S. et al.
 / TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
 / FILE REFERENCE: 38-21/(53452)B
 / CURRENT APPLICATION NUMBER: US/11/188,298
 / CURRENT FILING DATE: 2005-07-22
 / PRIOR APPLICATION NUMBER: 60/532,978
 / PRIOR FILING DATE: 2004-07-31
 / NUMBER OF SEQ ID NOS: 22569
 / SEQ ID NO: 21798
 / LENGTH: 557
 / TYPE: PRT
 / ORGANISM: Glycine max
 / FEATURE:
 / NAME/KEY: unsure
 / LOCATION: (1)-(557)
 / OTHER INFORMATION: unsure at all Xaa locations

RESULT 2
 US-11-188-298-21598 ; Query Match 21798, Score 66; DB 11; Length 557;
 Best Local Similarity 31.7%; Pred. No. 0.87%; Mismatches 9; Indels 2; Gaps 2;

Matches 19;	Conservative 19;	Mismatches 9;	Indels 2;	Gaps 2;
Qy	3 YYGTNGVHTCKNSLW-GKVRJRNMMYDQNT-TYMGRLQDILGWATGAFGKT 52			
Db	66 YETTELVHENKNGTQWVVKPKTVKFKTNTHVPKLGMLVGMGXGNNGST 117			

/ General Information:
 / Applicant: Abad, Mark S. et al.
 / Title of Invention: GENES AND USES FOR PLANT IMPROVEMENT
 / File Reference: 38-21/(53452)B
 / Current Application Number: US/11/188,298
 / Current Filing Date: 2005-07-22
 / Prior Application Number: 60/532,978
 / Prior Filing Date: 2004-07-31
 / Number of Seq Id Nos: 22569
 / Seq Id No: 21598

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; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 21598
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Sulfolobus solfataricus
US-11-188-21598

Query Match 21.5%; Score 65.5%; DB 11; Length 471;
Best Local Similarity 48.6%; Pred. No. 0.84;
Matches 17; Conservative 13; Indels 3; Gaps 2;
Qy 1 KTYGTN--GVHCTKNSLW-GKVRKMKYDQNTY 33
Db 255 KPIKGDNGTGGMH-THLSLWTKDGKKNLMDPNDYE 288

RESULT 3
US-11-188-298-13174
; Sequence 13174, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; CURRENT APPLICATION NUMBER: US/11/188,298
; FILE REFERENCE: 38-21(53452)B
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 13174
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Methanococcus voltae
US-11-188-298-13174

Query Match 20.6%; Score 62.5%; DB 11; Length 446;
Best Local Similarity 33.9%; Pred. No. 2;
Matches 19; Conservative 9; Mismatches 17; Indels 11; Gaps 5;
Qy 1 KTYGTN--GVHCTKNSLW-GKVRKMKYDQNTYMGRLQDILGWAFGKT 52
Db 237 KPFMNGSGMHNC-SIWLDGKPSF---YDENNAH-QSDICLSTYGGILBHT 285

RESULT 4
US-11-068-783-90
; Sequence 90, Application US/11068783
; Publication No. US20050260715A1
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Barfield, Daniel
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING
; CURRENT APPLICATION NUMBER: US/11/068,783
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/09/444,281
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Leuconostoc gelidum
US-11-068-783-90

Query Match 19.7%; Score 60.; DB 11; Length 37;
Best Local Similarity 48.4%; Pred. No. 0.26;
Matches 15; Conservative 2; Mismatches 4; Indels 10; Gaps 3;
Qy 3 YYGTTGNGVHCTKNSL--WGRKV-----RLRN 24
Db 2 YYG-NGVHCTKSGCSVANGEAFSAVGVRLLAN 31

RESULT 5
US-11-058-924-7
; Sequence 7, Application US/11058924
; Publication No. US20060019308A1
; GENERAL INFORMATION:
; APPLICANT: Lund, Frances E.
; TITLE OF INVENTION: CD38 MODULATED CHEMOTAXIS
; FILE REFERENCE: 13315/5
; CURRENT APPLICATION NUMBER: US/11/058,924
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 09/982,616
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/241,065
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-058-924-7

Query Match 19.7%; Score 60.; DB 11; Length 300;
Best Local Similarity 35.0%; Pred. No. 2.7;
Matches 14; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
Qy 5 GTINGVACPTNSLNGKVRKLMKQDNTYMGRLQDILGW 44
Db 113 GTQTPCNKILLWSRKLDAHQFTQVQRDMFTIEDTLIGY 152

RESULT 6
US-11-188-298-18003
; Sequence 18003, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abed, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 1003
; LENGTH: 670
; TYPE: PRT
; ORGANISM: GIBBERELLA ZEAE PH-1
US-11-188-298-18003

Query Match 18.9%; Score 57.5%; DB 11; Length 670;
Best Local Similarity 29.5%; Pred. No. 14;
Matches 13; Conservative 8; Mismatches 18; Indels 5; Gaps 2;
Qy 3 YYG-TTNGVHCTKNSLNGKVRKLMKQDNTYMGRLQDILGW 44
Db 566 YHGAVVNPIHL--SLWNERLGLGKSIDPEADWRKYQDMAEW 606

RESULT 7
US-11-188-298-15548
; Sequence 15548, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abed, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978

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PRIOR FILING DATE: 2004-07-31
 NUMBER OF SEQ ID NOS: 22569
 SEQ ID NO: 15548
 LENGTH: 473
 TYPE: PRT
 ORGANISM: Sulfolobus acidocaldarius
 US-11-188-298-15548

Query Match Score 57; DB 11; Length 473;
 Best Local Similarity 45.7%; Pred. No. 11; Indels 4; Gaps 3;
 Matches 16; Conservative 4; Mismatches 11;

Qy 1 KTYGGTN-GVHCTKNSLWGRVKRNMKYDONTY 33
 Db 257 KPFFGNGSGRH-TFDSLWTKDG-KNLMDPNDYE 299

RESULT 8
 US-11-188-298-9586
 Sequence 9586, Application US/111886298
 GENERAL INFORMATION:
 APPLICANT: Abad, Mark S. et al.
 TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
 FILE REFERENCE: 38-21(53452)B
 CURRENT APPLICATION NUMBER: US/11/188,298
 CURRENT FILING DATE: 2005-07-22
 PRIOR APPLICATION NUMBER: 60/592,978
 PRIOR FILING DATE: 2004-07-31
 NUMBER OF SEQ ID NOS: 22569
 SEQ ID NO: 9586
 LENGTH: 812
 TYPE: PRT
 ORGANISM: Eremotheicum gossypii
 US-11-188-298-9586

Query Match Score 56.5%; DB 11; Length 812;
 Best Local Similarity 29.4%; Pred. No. 24;
 Matches 15; Conservative 7; Mismatches 18; Indels 11; Gaps 1;

Qy 4 YGTNGVHCTKNSLWGRVKRNMKYDONTYMGRLQDILGWATGAFGKTFH 54
 Db 331 YGT-----GRAVLFEVSYQSNSWRYLBIVLYLIGAGGYGALFN 370

RESULT 9
 US-11-188-298-13006
 Sequence 13006, Application US/11188298
 GENERAL INFORMATION:
 APPLICANT: Abad, Mark S. et al.
 TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
 FILE REFERENCE: 38-21(53452)B
 CURRENT APPLICATION NUMBER: US/11/188,298
 CURRENT FILING DATE: 2005-07-22
 PRIOR APPLICATION NUMBER: 60/592,978
 NUMBER OF SEQ ID NOS: 22569
 SEQ ID NO: 13006
 LENGTH: 147
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE: NAME/KEY: unsure
 LOCATION: (1)-(147)
 OTHER INFORMATION: unsure at all Xaa locations
 US-11-188-298-13006

Query Match Score 56; DB 11; Length 147;
 Best Local Similarity 32.7%; Pred. No. 42;
 Matches 17; Conservative 10; Mismatches 23; Indels 2; Gaps 2;
 Qy 3 YYGTNGVHCTKNSLWGRVKRNMKYDONTYMGRLQDILGWATGAFGKT 52

RESULT 10
 US-11-188-298-15017
 Sequence 15017, Application US/11188298
 GENERAL INFORMATION:
 APPLICANT: Abad, Mark S. et al.
 TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
 FILE REFERENCE: 38-21(53452)B
 CURRENT APPLICATION NUMBER: US/11/188,298
 CURRENT FILING DATE: 2005-07-22
 PRIOR APPLICATION NUMBER: 60/592,978
 PRIOR FILING DATE: 2004-07-31
 NUMBER OF SEQ ID NOS: 22569
 SEQ ID NO: 15017
 LENGTH: 226
 TYPE: PRT
 ORGANISM: Glycine max
 US-11-188-298-15017

Query Match Score 55.5%; DB 11; Length 226;
 Best Local Similarity 36.5%; Pred. No. 7.9;
 Matches 19; Conservative 9; Mismatches 21; Indels 3; Gaps 3;

Qy 3 YYGTNGVHCTKNSLWGRVKRNMKYDONTYMGRLQDILGWATGAFGKT 52
 Db 26 YETTELVHENRNGTQWVVKPKTVYEFKTNTHVPLGMLVKG-GNNGST 76

RESULT 11
 US-10-915-002-299
 Sequence 299, Application US/10915002
 Publication No. US20060078950A1
 GENERAL INFORMATION:
 APPLICANT: Proguiske-Box, Ann
 APPLICANT: Hillman, Jeffrey D.
 APPLICANT: Handfield, Martin
 TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
 TITLE OF INVENTION: USE IN DIAGNOSIS ANTIGENS FOR USE IN THE DIAGNOSIS, TREATMENT, A
 TITLE OF INVENTION: PERIODONTAL DISEASES
 FILE REFERENCE: 02-042
 CURRENT APPLICATION NUMBER: US/10/915,002
 CURRENT FILING DATE: 2004-08-10
 NUMBER OF SEQ ID NOS: 354
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 299
 LENGTH: 480
 TYPE: PRT
 ORGANISM: Porphyromonas gingivalis
 US-10-915-002-299

Query Match Score 54.5%; DB 9; Length 480;
 Best Local Similarity 28.2%; Pred. No. 25;
 Matches 11; Conservative 12; Mismatches 13; Indels 3; Gaps 2;

Qy 3 YYGTNGVH--CTKNSL-WGKVRLKNMKYDQNTYMGRLQ 38
 Db 296 FYAKSGMHFYATKHNFWDKCSIKGMFLDRDKDLEGKMK 334

RESULT 12
 US-10-921-415-3
 Sequence 3, Application US/10921415
 Publication No. US20060014681A1
 GENERAL INFORMATION:
 APPLICANT: Chen, Xiaojiang
 APPLICANT: Holers, V. Michael
 TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND US
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: 2848-43

CURRENT APPLICATION NUMBER: US/10/921,415
 CURRENT FILING DATE: 2004-08-16
 PRIOR FILING DATE: US/09/834,309
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: Patentin version 3.0
 SEQ ID NO: 3
 LENGTH: 56
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-921-415-3

Query Match 17.6%; Score 53.5; DB 11; Length 278;
 Best Local Similarity 44.0%; Pred. No. 18;
 Matches 10; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

Qy 1 KTYGTNG--VHCTKNSLWGVRL
 Db 29 KTNFSMNGKSVWQANNMGPTRL 53

RESULT 15
 US-11-087-099-5419
 Sequence 5419, Application US/11087099
 Publication No. US20060041961A1
 GENERAL INFORMATION:
 APPLICANT: Abad, Mark S. et al.
 TITLE OF INVENTION: Genes and Uses for Plant Improvement
 FILE REFERENCE: 38-21(53450)B EP
 CURRENT APPLICATION NUMBER: US/11/087,099
 CURRENT FILING DATE: 2005-03-22
 NUMBER OF SEQ ID NOS: 12464
 SEQ ID NO 5419
 LENGTH: 353
 TYPE: PRT
 ORGANISM: Mesembranthemum crystallinum

US-11-087-099-5419

Query Match 17.6%; Score 53.5; DB 11; Length 353;
 Best Local Similarity 41.4%; Pred. No. 24;
 Matches 12; Conservative 4; Mismatches 8; Indels 5; Gaps 1;

Qy 24 NMKYDQNTYMGRLDIL----LGWATG 47
 Db 177 NIEMRNLVKAVIDFPRCQKGWATG 205

Search completed: May 2, 2006, 17:46:14
 Job time : 26 secs

RESULT 13
 US-10-921-415-4
 Sequence 4, Application US/10921415
 Publication No. US2006014681A1
 GENERAL INFORMATION:
 APPLICANT: Chen, Xiaojiang
 APPLICANT: Holers, V. Michael
 TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
 TITLE OF INVENTION: THEREOF
 FILE REFERENCE: 2848-43
 CURRENT APPLICATION NUMBER: US/10/921,415
 CURRENT FILING DATE: 2004-08-16
 PRIOR APPLICATION NUMBER: US/09/834,309
 PRIOR FILING DATE: 2001-04-11
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 4
 LENGTH: 134
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-921-415-4

Query Match 17.6%; Score 53.5; DB 9; Length 134;
 Best Local Similarity 44.0%; Pred. No. 8.1;
 Matches 11; Conservative 3; Mismatches 8; Indels 3; Gaps 1;

Qy 1 KTYGTNG--VHCTKNSLWGVRL
 Db 100 KTNFSMNGKSVWQANNMGPTRL 124

RESULT 14
 US-11-087-099-587
 Sequence 587, Application US/11087099
 Publication No. US20060041961A1
 GENERAL INFORMATION:
 APPLICANT: Abad, Mark S. et al.
 TITLE OF INVENTION: Genes and Uses for Plant Improvement
 FILE REFERENCE: 38-21(53450)B EP
 CURRENT APPLICATION NUMBER: US/11/087,099
 CURRENT FILING DATE: 2005-03-22
 NUMBER OF SEQ ID NOS: 12464
 SEQ ID NO 587
 LENGTH: 278
 TYPE: PRT
 ORGANISM: Oryza sativa
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(278)
 OTHER INFORMATION: unsure at all xaa locations

US-11-087-099-587